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PA (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-367863/38.
 XX
 PT Identifying complementary peptides by analysis of protein and
 PT nucleotide sequence databases, useful in drug design -
 XX
 PS Example 5; Page 385; 488pp; English.
 XX
 CC The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryote genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 20; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 DB 6 DLDA 9
 RESULT 19
 AAB46866
 ID AAB46866 standard; peptide; 10 AA.
 XX
 AC AAB46866;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #5.
 XX
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
 KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
 KW vulnary; cerebroprotective; antiangiinal; antidiabetic; nephrotropic;
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;
 KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 9 /label= Abu
 FT /note= "2-aminobutyric acid"
 FT Modified-site 10 /label= Abu
 FT /note= "2-aminobutyric acid"
 FT
 XX DE19933173-A1.
 XX
 XX 18-JAN-2001.
 PD
 XX 15-JUL-1999; 99DE-1033173.
 PF
 XX 15-JUL-1999; 99DE-1033173.
 PR
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Jonczyk A, Diefenbach B, Goodman S;
 FI
 XX

DR WPI; 2001-192448/20.
 XX
 PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
 PT useful e.g. for treating thrombosis, coronary heart disease, tumors,
 PT osteoporosis, inflammation or infections -
 XX
 PS Claim 3; Page 5; 20pp; German.
 XX
 CC This invention describes novel cyclic peptides (I), containing 8 amino
 CC acid residues and optionally further alpha,omega-aminocarboxylic acid
 CC residues. Cyclic peptides of formula Cyclo-(Arg-X₁-Asp-X₂-X₃-X₄-
 CC X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
 CC X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
 CC Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, His or
 CC Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
 CC length of 50-2500 nm; or is absent; the amino acid residues are
 CC optionally derivatized and include D- as well as L-forms (in the case of
 CC optically active aminoacids). The products of the invention have
 CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
 CC antiinflammatory, antibacterial, antipsoriatic, vulnary,
 CC cerebroprotective, antiangiinal, antidiabetic, ophthalmological,
 CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
 CC neuroprotective. (I) are used for treating diseases involving expression
 CC and pathological function of alpha_vbeta_6-integrin receptors, especially
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 CC wound healing deficiency. Other disclosed disorders to be treated include
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
 CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 CC rhebetic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
 CC also be useful in analytical biology and molecular biology; e.g.
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 CC used to prepare affinity chromatography columns for purifying integrins.
 CC DNA encoding (I) may be used for treating the same disorders as (I)
 CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 CC receptor inhibiting activity.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 20; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 DB 3 DLDA 6
 RESULT 20
 AAB46867
 ID AAB46867 standard; peptide; 10 AA.
 XX
 AC AAB46867;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #6.
 XX
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
 KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
 KW vulnary; cerebroprotective; antiangiinal; antidiabetic; nephrotropic;
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;
 KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "D-form residue"
 FT

FT Modified-site 9 /label= Aha
 FT /note= "6-aminohexanoic acid"
 FT 10
 FT Modified-site
 FT /label= Aha
 FT /note= "6-aminohexanoic acid"
 XX
 PN DE19933173-A1.
 XX
 XX 18-JAN-2001.
 PD
 PD 15-JUL-1999; 99DE-1033173.
 PF
 PF 15-JUL-1999; 99DE-1033173.
 PR
 XX (MERE) MERCK PATENT GMBH.
 XX
 PA Jonczyk A, Diefenbach B, Goodman S;
 PI WPI; 2001-192448/20.
 XX
 DR
 XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
 FT useful e.g. for treating thrombosis, coronary heart disease, tumors,
 FT osteoporosis, inflammation or infections
 PT
 PT
 PS Claim 3; Page 5; 20pp; German.
 XX
 CC This invention describes novel cyclic peptides (I), containing 8 amino
 CC acid residues and optionally further alpha,omega-aminocarboxylic acid
 CC residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-
 CC X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
 CC X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
 CC Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
 CC Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
 CC length of 50-2500 mum; or is absent; the amino acid residues are
 CC optionally derivatized and include D- as well as L-forms (in the case of
 CC optically active aminoacids). The products of the invention have
 CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
 CC antiinflammatory, antibacterial, antipsoriatic, vulnerary,
 CC cerebroprotective, antianginal, antidiabetic, ophthalmological,
 CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
 CC neuroprotective. (I) are used for treating diseases involving expression
 CC and pathological function of alpha_vbeta_6-integrin receptors, especially
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 CC wound healing deficiency. Other disclosed disorders to be treated include
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
 CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 CC rubrotoxic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
 CC also be useful in analytical biology and molecular biology; e.g.
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 CC used to prepare affinity chromatography columns for purifying integrins.
 CC DNA encoding (I) may be used for treating the same disorders as (I)
 CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 CC receptor inhibiting activity.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 20; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 3 DLDA 6
 RESULT 21
 AAB46870
 ID AAB46870 standard; peptide: 10 AA.
 XX

AC
 XX
 DT
 XX
 DE
 XX
 XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #9.
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
 KW cystostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
 KW vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic;
 KW ophthalmological; antiarthritic; antirheumatic; antitumor; vasotropic;
 KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 9 /label= Abu
 FT /note= "2-aminobutyric acid"
 FT Modified-site 10 /label= Abu
 FT /note= "2-aminobutyric acid"
 FT
 XX DE19933173-A1.
 XX
 XX 18-JAN-2001.
 PD
 PD 15-JUL-1999; 99DE-1033173.
 PF
 PF 15-JUL-1999; 99DE-1033173.
 PR
 PR (MERE) MERCK PATENT GMBH.
 XX
 PA Jonczyk A, Diefenbach B, Goodman S;
 PI WPI; 2001-192448/20.
 XX
 DR New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
 FT useful e.g. for treating thrombosis, coronary heart disease, tumors,
 FT osteoporosis, inflammation or infections
 PT
 PT
 PS Claim 3; Page 5; 20pp; German.
 XX
 CC This invention describes novel cyclic peptides (I), containing 8 amino
 CC acid residues and optionally further alpha,omega-aminocarboxylic acid
 CC residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-
 CC X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
 CC X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
 CC Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
 CC Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
 CC length of 50-2500 mum; or is absent; the amino acid residues are
 CC optionally derivatized and include D- as well as L-forms (in the case of
 CC optically active aminoacids). The products of the invention have
 CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
 CC antiinflammatory, antibacterial, antipsoriatic, vulnerary,
 CC cerebroprotective, antianginal, antidiabetic, ophthalmological,
 CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
 CC neuroprotective. (I) are used for treating diseases involving expression
 CC and pathological function of alpha_vbeta_6-integrin receptors, especially
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 CC wound healing deficiency. Other disclosed disorders to be treated include
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
 CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 CC rubrotoxic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
 CC also be useful in analytical biology and molecular biology; e.g.
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 CC used to prepare affinity chromatography columns for purifying integrins.
 CC DNA encoding (I) may be used for treating the same disorders as (I)
 CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 CC receptor inhibiting activity.
 XX

CC DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin receptor inhibiting activity.

XX Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

RESULT 22

AAB46885

ID AAB46885 standard; peptide; 10 AA.

XX AC AAB46885;

XX DT 09-MAY-2001 (first entry)

XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #17.

XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;

XX cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

XX vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;

XX ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

XX neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;

XX cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;

XX osteoporosis; inflammation; infection; psoriasis; wound healing.

XX OS Synthetic.

XX FH Key

FT Misc-difference 5

FT Location/Qualifiers

FT /note= "D-form residue"

XX DE19933173-Al.

XX 18-JAN-2001.

XX 15-JUL-1999; 99DE-1033173.

XX 15-JUL-1999; 99DE-1033173.

XX (MERE) MERCK PATENT GMBH.

XX Jonczyk A, Diefenbach B, Goodman S;

XX WPI; 2001-192448/20.

XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections

XX Example 1; Page 10; 20pp; German.

XX This invention describes novel cyclic peptides (I), containing 8 amino acid residues and optionally further alpha,omega-aminocarboxylic acid residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;

XX X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ = Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or

XX Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a length of 50-2500 mum; or is absent; the amino acid residues are

XX optionally derivatized and include D- as well as L-forms (in the case of optically active aminoacids). The products of the invention have

XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic, CC antiinflammatory, antibacterial, antipsoriatic, vulnary,

XX cerebroprotective, antianginal, antidiabetic, ophthalmological, CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,

CC neuroprotective. (I) are used for treating diseases involving expression and pathological function of alpha_vbeta_6-integrin receptors, especially CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and wound healing deficiency. Other disclosed disorders to be treated include CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic retinopathy, macular degeneration, myopia, ocular histioplasmosis or CC rubenotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, CC acute renal failure, renal inflammation or multiple sclerosis. (I) may also be useful in analytical biology and molecular biology; e.g. CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be used to prepare affinity chromatography columns for purifying integrins.

CC DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin receptor inhibiting activity.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

RESULT 23

AAB46862

ID AAB46862 standard; peptide; 11 AA.

XX AC AAB46862;

XX DT 09-MAY-2001 (first entry)

XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #1.

XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;

XX cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

XX vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;

XX ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

XX neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;

XX cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;

XX osteoporosis; inflammation; infection; psoriasis; wound healing.

XX OS Synthetic.

XX DE19933173-Al.

XX 18-JAN-2001.

XX 15-JUL-1999; 99DE-1033173.

XX 15-JUL-1999; 99DE-1033173.

XX (MERE) MERCK PATENT GMBH.

XX Jonczyk A, Diefenbach B, Goodman S;

XX WPI; 2001-192448/20.

XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections

XX Claim 3; Page 5; 20pp; German.

XX This invention describes novel cyclic peptides (I), containing 8 amino acid residues and optionally further alpha,omega-aminocarboxylic acid residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;

XX X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ = Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Lys or Phe;

XX R₁ = one or more omega-aminocarboxylic acid residues, having a length of 50-2500 mum; or is absent; the amino acid residues are

XX optionally derivatized and include D- as well as L-forms (in the case of optically active aminoacids). The products of the invention have

XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic, CC antiinflammatory, antibacterial, antipsoriatic, vulnary,

XX cerebroprotective, antianginal, antidiabetic, ophthalmological, CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,

CC Gly, Ala or Ser; X_5 = Leu, Ile, Nle, Val or Phe; X_6 = Arg, Har or
 CC Lys; R_1 = one or more omega-aminocarboxylic acid residues, having a
 CC length of 50-2500 mum; or is absent; the amino acid residues are
 CC optionally derivatized and include D- as well as L-forms (in the case of
 CC optically active aminoacids). The products of the invention have
 CC antithrombotic, cardiant, antiarteriosclerotic, cyostatic, osteopathic,
 CC antiinflammatory, antibacterial, antiarteriosclerotic, osteopathic,
 CC cerebroprotective, antianginal, antidiabetic, ophthalmological,
 CC antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic,
 CC neuroprotective. (I) are used for treating diseases involving expression
 CC and pathological function of alpha_vbeta_6-integrin receptors, especially
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 CC wound healing deficiency. Other disclosed disorders to be treated include
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
 CC retinopathy, macular degeneration, myopia, ocular histioplasmosis or
 CC rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
 CC also be useful in analytical biology and molecular biology; e.g.
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 CC used to prepare affinity chromatography columns for purifying integrins.
 CC DNA encoding (I) may be used for treating the same disorders as (I)
 CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 CC receptor inhibiting activity.
 CC
 CC Sequence 11 AA;
 CC
 CC Query Match 100.0%; Score 20; DB 22; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DLDA 4
 CC Db 3 DLDA 6
 CC
 CC RESULT 24
 CC AAB46865
 CC ID AAB46865 standard; peptide; 11 AA.
 CC
 CC AC AAB46865;
 CC
 CC DT 09-MAY-2001 (first entry)
 CC
 CC DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #4.
 CC
 CC KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
 CC cyostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
 CC vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic;
 CC ophthalmological; antiarthritic; antirheumatic; antitumor; vasotropic;
 CC neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
 CC cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
 CC osteoporosis; inflammation; infection; psoriasis; wound healing.
 CC
 CC OS Synthetic.
 CC
 CC FH Key Location/Qualifiers
 CC FT Misc-difference 5 /note= "D-form residue"
 CC FT
 CC
 CC PN DE19933173-A1.
 CC
 CC XX 18-JAN-2001.
 CC
 CC PF 15-JUL-1999; 99DE-1033173.
 CC
 CC XX 15-JUL-1999; 99DE-1033173.
 CC
 CC XX (MERE) MERCK PATENT GMBH.
 CC
 CC XX Jonczyk A, Diefenbach B, Goodman S;
 CC PI
 CC PD 18-JAN-2001.

WPI; 2001-192448/20.

New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections -

Claim 3; Page 5; 20pp; German.

This invention describes novel cyclic peptides (I), containing 8 amino acid residues and optionally further alpha,omega-aminocarboxylic acid residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr; X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ = Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a length of 50-2500 mum; or is absent; the amino acid residues are optionally derivatized and include D- as well as L-forms (in the case of optically active aminoacids). The products of the invention have antithrombotic, cardiant, antiarteriosclerotic, cyostatic, osteopathic, antiinflammatory, antibacterial, antiarteriosclerotic, vasotrophic, cerebroprotective, antianginal, antidiabetic, ophthalmological, antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic, neuroprotective. (I) are used for treating diseases involving expression and pathological function of alpha_vbeta_6-integrin receptors, especially thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and wound healing deficiency. Other disclosed disorders to be treated include apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic retinopathy, macular degeneration, myopia, ocular histioplasmosis or rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, acute renal failure, renal inflammation or multiple sclerosis. (I) may also be useful in analytical biology and molecular biology; e.g. fluorescently labeled (I) may be used as diagnostic markers or (I) may be used to prepare affinity chromatography columns for purifying integrins. DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha_vbeta_6-integrin receptor inhibiting activity.

SQ Sequence 11 AA;

Query Match 100.0%; Score 20; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

Db 3 DLDA 6

RESULT 25

AAB46875

ID AAB46875 standard; peptide; 11 AA.

AC AAB46875;

XX

XX

DT 09-MAY-2001 (first entry)

XX

DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor SEQ ID 3.

XX

KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;

KW cyostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

KW vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic;

KW ophthalmological; antiarthritic; antirheumatic; antitumor; vasotropic;

KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;

KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;

KW osteoporosis; inflammation; infection; psoriasis; wound healing.

XX

OS Synthetic.

XX

XX DE19933173-A1.

XX

XX 18-JAN-2001.

PD

XX 15-JUL-1999; 99DE-1033173.
 XX 15-JUL-1999; 99DE-1033173.
 XX (MERE) MERCK PATENT GMBH.
 XX Jonczyk A, Diefenbach B, Goodman S;
 XX WPI; 2001-192448/20.
 XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
 XX useful e.g. for treating thrombosis, coronary heart disease, tumors,
 XX osteoporosis, inflammation or infections
 XX Examples; Page 16; 20pp; German.
 XX This invention describes novel cyclic peptides (I), containing 8 amino
 XX acid residues and optionally further alpha,omega-aminocarboxylic acid
 XX residues. Cyclic peptides of formula Cyclo-(Arg-X₁-Asp-X₂-X₃-X₄-
 XX X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
 XX X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
 XX Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
 XX Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
 XX length of 50-2500 mum; or is absent; the amino acid residues are
 XX optionally derivatized and include D- as well as L-forms (in the case of
 XX optically active aminoacids). The products of the invention have
 XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
 XX antiinflammatory, antibacterial, antiarteriosclerotic, vasotrophic,
 XX cerebroprotective, antianginal, antidiabetic, ophthalmological,
 XX antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
 XX neuroprotective. (I) are used for treating diseases involving expression
 XX and pathological function of alpha_vbeta_6-integrin receptors, especially
 XX thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 XX tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 XX wound healing deficiency. Other disclosed disorders to be treated include
 XX apoplexy, angina pectoris, rheumatoid arthritis, osteoarthritis, ulcerative
 XX retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 XX colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 XX acute renal failure, renal inflammation or multiple sclerosis. (I) may
 XX also be useful in analytical biology and molecular biology; e.g.
 XX fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 XX used to prepare affinity chromatography columns for purifying integrins.
 XX DNA encoding (I) may be used for treating the same disorders as (I)
 XX itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 XX receptor inhibiting activity.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 20; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 3 DLDA 6
 RESULT 26
 AAB46878
 ID AAB46878 standard; peptide; 11 AA.
 XX AAB46878;
 AC
 XX 09-MAY-2001 (first entry)
 DT Integrin alpha-Vbeta-6 cyclic peptide inhibitor SEQ ID 6.
 DE
 XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
 KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
 KW vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic;
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.
 XX Synthetic.
 OS DEL9933173-AL.
 XX
 PN 18-JAN-2001.
 XX
 PD 15-JUL-1999; 99DE-1033173.
 XX
 PF 15-JUL-1999; 99DE-1033173.
 XX
 PR 15-JUL-1999; 99DE-1033173.
 XX
 XX (MERE) MERCK PATENT GMBH.
 XX
 XX Jonczyk A, Diefenbach B, Goodman S;
 XX WPI; 2001-192448/20.
 XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
 XX useful e.g. for treating thrombosis, coronary heart disease, tumors,
 XX osteoporosis, inflammation or infections
 XX Examples; Page 17; 20pp; German.
 XX This invention describes novel cyclic peptides (I), containing 8 amino
 XX acid residues and optionally further alpha,omega-aminocarboxylic acid
 XX residues. Cyclic peptides of formula Cyclo-(Arg-X₁-Asp-X₂-X₃-X₄-
 XX X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
 XX X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
 XX Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
 XX Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
 XX length of 50-2500 mum; or is absent; the amino acid residues are
 XX optionally derivatized and include D- as well as L-forms (in the case of
 XX optically active aminoacids). The products of the invention have
 XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
 XX antiinflammatory, antibacterial, antiarteriosclerotic, vasotrophic,
 XX cerebroprotective, antianginal, antidiabetic, ophthalmological,
 XX antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
 XX neuroprotective. (I) are used for treating diseases involving expression
 XX and pathological function of alpha_vbeta_6-integrin receptors, especially
 XX thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
 XX tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
 XX wound healing deficiency. Other disclosed disorders to be treated include
 XX apoplexy, angina pectoris, rheumatoid arthritis, osteoarthritis, ulcerative
 XX retinopathy, macular degeneration, myopia, ocular histoplasmosis or
 XX colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
 XX acute renal failure, renal inflammation or multiple sclerosis. (I) may
 XX also be useful in analytical biology and molecular biology; e.g.
 XX fluorescently labeled (I) may be used as diagnostic markers or (I) may be
 XX used to prepare affinity chromatography columns for purifying integrins.
 XX DNA encoding (I) may be used for treating the same disorders as (I)
 XX itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
 XX receptor inhibiting activity.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 20; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 3 DLDA 6
 RESULT 27
 AAB46887
 ID AAB46887 standard; peptide; 11 AA.
 XX AAB46887;
 AC

XX 09-MAY-2001 (first entry)
XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #19.
XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
KW cystostatic; osteopathic; antinflammatory; antibacterial; antipsoriatic;
KW vulnary; cerebroprotective; antiangular; antidiabetic; nephrotropic;
KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;
KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
KW osteoporosis; inflammation; infection; psoriasis; wound healing.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 5 /note= "D-form residue"
FT
FT
XX DE19933173-AL.
XX 18-JAN-2001.
XX 15-JUL-1999; 99DE-1033173.
XX 15-JUL-1999; 99DE-1033173.
XX (MERE) MERCK PATENT GMBH.
XX Joneczyk A, Diefenbach B, Goodman S;
PI WPI; 2001-192448/20.
XX
XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
PT useful e.g. for treating thrombosis, coronary heart disease, tumors,
PT osteoporosis, inflammation or infections
XX Example 1; Page 11; 20pp; German.
XX
XX This invention describes novel cyclic peptides (I), containing 8 amino
CC acid residues and optionally further alpha,omega-aminocarboxylic acid
CC residues. Cyclic peptides of formula Cyclo-(Arg-X₁-Asp-X₂-X₃-X₄-
CC X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
CC X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
CC Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
CC Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
CC length of 50-2500 mum; or is absent; the amino acid residues are
CC optionally derivatized and include D- as well as L-forms (in the case of
CC optically active aminoacids). The products of the invention have
CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
CC antiinflammatory, antibacterial, antipsoriatic, vulnary,
CC cerebroprotective, antiangular, antidiabetic, ophthalmological,
CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
CC neuroprotective. (I) are used for treating diseases involving expression
CC and pathological function of alpha_vbeta_6-integrin receptors, especially
CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
CC wound healing deficiency. Other disclosed disorders to be treated include
CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
CC rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
CC also be useful in analytical biology and molecular biology; e.g.
CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
CC used to prepare affinity chromatography columns for purifying integrins.
CC DNA encoding (I) may be used for treating the same disorders as (I)
CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
CC receptor inhibiting activity.
XX Sequence 11 AA;

Query Match 100.0%; Score 20; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
DB 3 DLDA 6
RESULT 28
AAR97407
ID AAR97407 standard; peptide; 12 AA.
XX
AC AAR97407;
DT 02-DEC-1996 (first entry)
XX
DE Streptococcal M protein peptide, p145, fragment J(1)1.
XX
KW Streptococcal; M protein; peptide; p145; chimeric; chimeric;
KW B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW detection; mapping; opsonic antibody; vaccine;
KW group A Streptococci; immunotherapy; diagnosis.
XX
OS Streptococcus spp.
XX
XX WO9611944-A1.
XX
PD 25-APR-1996.
XX
PF 16-OCT-1995; 95WO-AU00681.
XX
PR 14-OCT-1994; 94AU-0008851.
XX
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (COUN) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSLC-) CSL LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (UYME) UNIV MELBOURNE.
XX
PI Cooper JA, Good MF, Relf WA, Saul AJ;
XX WPI; 1996-221939/22.
DR
XX New chimaeric peptide(s) including a conformational epitope -
PT inserted into a peptide having similar native conformation, useful
PT in vaccines and for determin. of minimal epitope(s) or for mapping
PT amphipathic helices
XX
XX Example 13; Page 37; 99pp; English.
PS
XX The present peptide is a fragment of the streptococcal M protein
CC peptide p145 (Pruksakorn et al, J. Immunol. 149: 2739-2735 (1992)),
CC used in the construction of a novel chimaeric peptide (CP). The CP
CC comprises a B-cell conformational epitope from within p145,
CC inserted into a 2nd peptide, pref. an alpha-helical coil based on
CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
CC similar conformation, enabling the epitope to be presented in an
CC immunologically active conformation.
CC The CP can be used in a novel detection/mapping process, e.g. to
CC determine the min. epitope required to induce opsonic antibodies
CC (Ab), and in vaccines against gp. A Streptococci. Ab raised against
CC the CP can be used for immunotherapy and diagnosis, while the CP
CC can be used diagnostically to detect Ab.
XX
XX Sequence 12 AA;
SQ
Query Match 100.0%; Score 20; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
DB 3 DLDA 6

```
Db      4 DLDA 7

RESULT 29
AAR97408
ID      AAR97408 standard; peptide; 12 AA.
XX
AC      AAR97408;
XX
XX      02-DEC-1996 (first entry)
XX
DE      Streptococcal M protein peptide, p145, fragment J(I)2.
XX
KW      Streptococcal; M protein; peptide; p145; chimaeric; chimeric;
KW      B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW      detection; mapping; opsonic antibody; vaccine;
KW      group A Streptococci; immunotherapy; diagnosis.
XX
OS      Streptococcus spp.
XX
PN      WO9611944-A1.
XX
PD      25-APR-1996.
XX
PF      16-OCT-1995; 95WO-AU00681.
XX
PR      14-OCT-1994; 94AU-0008851.
XX
PA      (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA      (CSLC-) CSL LTD.
PA      (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA      (UYME ) UNIV MELBOURNE.
XX
PI      Cooper JA, Good MF, Relf WA, Saul AJ;
XX      WPI; 1996-221939/22.
XX
XX      New chimaeric peptide(s) including a conformational epitope -
PT      inserted into a peptide having similar native conformation, useful
PT      in vaccines and for determin. of minimal epitope(s) or for mapping
PT      amphipathic helices
XX
XX      Example 13; Page 37; 99pp; English.
XX
CC      The present peptide is a fragment of the Streptococcal M protein
CC      peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),
CC      used in the construction of a novel chimaeric peptide (CP). The CP
CC      comprises a B-cell conformational epitope from within p145,
CC      inserted into a 2nd peptide, pref. an alpha-helical coil based on
CC      the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
CC      similar conformation, enabling the epitope to be presented in an
CC      immunologically active conformation.
CC      The CP can be used in a novel detection/mapping process, e.g. to
CC      determine the min. epitope required to induce opsonic antibodies
CC      (Ab), and in vaccines against gp. A Streptococci. Ab raised against
CC      the CP can be used for immunotherapy and diagnosis, while the CP
CC      can be used diagnostically to detect Ab.
XX
SQ      Sequence 12 AA;

      Query Match      100.0%; Score 20; DB 17; Length 12;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DLDA 4
      |||
Db      3 DLDA 6

RESULT 30
AAR97409
ID      AAR97409 standard; peptide; 12 AA.
XX
AC      AAR97409;
XX
XX      02-DEC-1996 (first entry)
XX
DE      Streptococcal M protein peptide, p145, fragment J(I)3.
XX
KW      Streptococcal; M protein; peptide; p145; chimaeric; chimeric;
KW      B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW      detection; mapping; opsonic antibody; vaccine;
KW      group A Streptococci; immunotherapy; diagnosis.
XX
OS      Streptococcus spp.
XX
PN      WO9611944-A1.
XX
PD      25-APR-1996.
XX
PF      16-OCT-1995; 95WO-AU00681.
XX
PR      14-OCT-1994; 94AU-0008851.
XX
PA      (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA      (CSLC-) CSL LTD.
PA      (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA      (UYME ) UNIV MELBOURNE.
XX
PI      Cooper JA, Good MF, Relf WA, Saul AJ;
XX      WPI; 1996-221939/22.
XX
XX      New chimaeric peptide(s) including a conformational epitope -
PT      inserted into a peptide having similar native conformation, useful
PT      in vaccines and for determin. of minimal epitope(s) or for mapping
PT      amphipathic helices
XX
XX      Example 13; Page 37; 99pp; English.
XX
CC      The present peptide is a fragment of the Streptococcal M protein
CC      peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),
CC      used in the construction of a novel chimaeric peptide (CP). The CP
CC      comprises a B-cell conformational epitope from within p145,
CC      inserted into a 2nd peptide, pref. an alpha-helical coil based on
CC      the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
CC      similar conformation, enabling the epitope to be presented in an
CC      immunologically active conformation.
CC      The CP can be used in a novel detection/mapping process, e.g. to
CC      determine the min. epitope required to induce opsonic antibodies
CC      (Ab), and in vaccines against gp. A Streptococci. Ab raised against
CC      the CP can be used for immunotherapy and diagnosis, while the CP
CC      can be used diagnostically to detect Ab.
XX
SQ      Sequence 12 AA;

      Query Match      100.0%; Score 20; DB 17; Length 12;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 DLDA 4
      |||
Db      3 DLDA 6

RESULT 31
AAR97410
ID      AAR97410 standard; peptide; 12 AA.
XX
AC      AAR97410;
XX
XX      02-DEC-1996 (first entry)
XX
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XX DE Streptococcal M protein peptide, p145, fragment J(I)4.
XX KW Streptococcal; M protein; peptide; p145; chimaeric; chimeric;
KW B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW detection; mapping; opsonic antibody; vaccine;
KW group A Streptococci; immunotherapy; diagnosis.
XX OS Streptococcus spp.
XX FH WO9611944-A1.
XX FT 25-APR-1996.
XX XX 16-OCT-1995; 95WO-AU00681.
XX PF 14-OCT-1994; 94AU-0008851.
XX PR (BIOT-) BIOTECH AUSTRALIA PTY LTD.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX PA (CSLC-) CSL LTD.
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX PA (UYME) UNIV MELBOURNE.
XX PI Cooper JA, Good MF, Relf WA, Saul AJ;
XX WPI; 1996-221939/22.
XX XX New chimaeric peptide(s) including a conformational epitope -
XX PT inserted into a peptide having similar native conformation, useful
XX PT in vaccines and for determin. of minimal epitope(s) or for mapping
XX PT amphipathic helices
XX XX Example 13; Page 37; 99pp; English.
XX CC The present peptide is a fragment of the Streptococcal M protein
XX CC peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),
XX CC used in the construction of a novel chimaeric peptide (CP). The CP
XX CC comprises a B-cell conformational epitope from within p145,
XX CC inserted into a 2nd peptide, pref. an alpha-helical coil based on
XX CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
XX CC similar conformation, enabling the epitope to be presented in an
XX CC immunologically active conformation.
XX CC The CP can be used in a novel detection/mapping process, e.g. to
XX CC determine the min. epitope required to induce opsonic antibodies
XX CC (Ab), and in vaccines against gp. A Streptococci. Ab raised against
XX CC the CP can be used for immunotherapy and diagnosis, while the CP
XX CC can be used diagnostically to detect Ab.
XX SQ Sequence 12 AA;
XX Query Match 100.0%; Score 20; DB 17; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 D LDA 4
XX I I I I
XX Db 1 D LDA 4
XX RESULT 32
XX AAB46888
XX ID AAB46888 standard; peptide; 12 AA.
XX AC AAB46888;
XX XX 09-MAY-2001 (first entry)
XX XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #20.
XX KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
XX KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

```

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KW KW vulnery; cerebroprotective; antianigmal; antidiabetic; nephrotropic;
KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;
KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
KW osteoporosis; inflammation; infection; psoriasis; wound healing.
XX OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 5 /note= "D-form residue"
XX DE19933173-A1.
XX 18-JAN-2001.
XX 15-JUL-1999; 99DE-1033173.
XX 15-JUL-1999; 99DE-1033173.
XX (MERE) MERCK PATENT GMBH.
XX Jonczyk A, Diefenbach B, Goodman S;
XX WPI; 2001-192448/20.
XX XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
XX useful e.g. for treating thrombosis, coronary heart disease, tumors,
XX osteoporosis, inflammation or infections -
XX Example 1; Page 11; 20pp; German.
XX CC This invention describes novel cyclic peptides (I), containing 8 amino
XX CC acid residues and optionally further alpha,omega-amino-carboxylic acid
XX CC residues. Cyclic peptides of formula Cyclo-(Arg-X1-Asp-X2-X3-X4-
XX CC X5-X6-R1) (I) and their salts and solvates. X1 = Ser, Gly or Thr;
XX CC X2 = Leu, Ile, Nle, Val or Phe; X3 = Asp, Glu, Lys or Phe; X4 =
XX CC Gly, Ala or Ser; X5 = Leu, Ile, Nle, Val or Phe; X6 = Arg, Har or
XX CC Lys; R1 = one or more omega-amino-carboxylic acid residues, having a
XX CC length of 50-2500 mum; or is absent; the amino acid residues are
XX CC optionally derivatized and include D- as well as L-forms (in the case of
XX CC optically active aminoacids). The products of the invention have
XX CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
XX CC antiinflammatory, antibacterial, antipsoriatic, vulnery,
XX CC cerebroprotective, antianigmal, antidiabetic, ophthalmological,
XX CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
XX CC neuroprotective. (I) are used for treating diseases involving expression
XX CC and pathological function of alpha_vbeta_6-integrin receptors, especially
XX CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
XX CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
XX CC wound healing deficiency. Other disclosed disorders to be treated include
XX CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
XX CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
XX CC rubecotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
XX CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
XX CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
XX CC also be useful in analytical biology and molecular biology; e.g.
XX CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
XX CC used to prepare affinity chromatography columns for purifying integrins.
XX CC DNA encoding (I) may be used for treating the same disorders as (I)
XX CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
XX CC receptor inhibiting activity.
XX SQ Sequence 12 AA;
XX Query Match 100.0%; Score 20; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 D LDA 4
XX I I I I
XX Db 3 D LDA 6

```

```
RESULT 33
AAW72284
ID AAW72284 standard; peptide; 13 AA.
XX
XX
AC AAW72284;
XX
XX DT 16-DEC-1998 (first entry)
XX
XX Dermatophagoides Der p I protein peptide DPI-26.3.
XX
XX genus Dermatophagoides; major protein allergen; T cell epitope;
KW Der p I; Der p II; Der f I; Der f II; house dust mite allergy.
XX
XX Dermatophagoides sp.
XX
XX US5820862-A.
XX
XX DT 13-OCT-1998.
XX
XX PF 07-JUN-1995; 95US-0482142.
XX
XX PR 19-MAY-1995; 95US-0445307.
XX
XX PR 14-APR-1994; 94US-0227772.
XX
XX PR 07-JUN-1995; 95US-0482142.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Chen X, Evans S, Franzen HM, Garman RD, Greenstein JL;
PI Kuo M, Rogers BL, Shaked Z;
XX WPI; 1998-567590/48.
XX
XX Dermatophagoides allergen peptides - useful for treating house dust
PT mite allergy
PT
XX Disclosure; Column 145-146; 155pp; English.
XX
XX The present invention describes peptides for treating sensitivity to
CC house dust mite allergens from the genus Dermatophagoides. Peptides
CC within the scope of the invention comprise at least one T cell epitope,
CC or preferably at least two T cell epitopes of a protein allergen
CC selected from the allergens Der p I, Der p II, Der f I, or Der f II.
CC The invention also describes modified peptides having similar or
CC enhanced therapeutic properties as the corresponding, naturally
CC occurring allergen, but having reduced side effects. AAW71912 to
CC AAW72000, and AAW72257 to AAW72330 represent peptides from the present
CC invention.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 20; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 5 DLDA 8
|||||

RESULT 34
AAW50486
ID AAY50486 standard; Peptide; 13 AA.
XX
XX AC AAY50486;
XX
XX DT 25-JAN-2000 (first entry)
XX
XX Dermatophagoides sp major protein allergen DP I-26.3.
XX
XX Allergen; house dust mite; detection; sensitivity; T cell epitope;
KW screening; allergic disorder; asthma; rhinitis; ectopic dermatitis;
KW Der f I; Der p I; Der p II; Der f II.
```

```
XX
OS Dermatophagoides sp.
XX
XX US5968526-A.
XX
XX PD 19-OCT-1999.
XX
XX PF 07-JUN-1995; 95US-0478572.
XX
XX PR 19-MAY-1995; 95US-0445307.
XX
XX PR 14-APR-1994; 94US-0227772.
XX
XX PR 12-APR-1995; 95WO-US04481.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Garman RD, Greenstein JL, Rogers BL, Franzen HM, Shaked Z, Chen X;
PI Evans S, Kuo M;
XX
XX WPI; 1999-590385/50.
XX
XX Screening individuals for allergic reactions to T cell epitopes of
PT major allergens from house dust mites -
PT
XX Claim 5w; Column 145-146; 158pp; English.
XX
XX This invention describes a novel method (I) for detecting whether an
CC individual is sensitive to Dermatophagoides (house dust mites). The
CC method involves detecting sensitivity to house dust mites in patients,
CC comprising combining a blood sample from the individual with 1 or more
CC isolated T cell epitopes of the protein allergens I and II (DP I) and
CC (DP II) from Dermatophagoides (house dust mites). 32 T cell epitopes
CC with varying, defined amino acids sequences (given in the specification)
CC may be used in (I). The sample and allergens are combined under
CC conditions appropriate for the binding of blood components with the
CC polypeptides. The extent of binding is then indicative of the
CC sensitivity of the patient to house dust mites. (I) may be used to screen
CC individuals for sensitivity to Dermatophagoides (house dust mites). The
CC house dust mite is a major cause of a variety of allergic disorders such
CC as asthma, rhinitis and ectopic dermatitis. AAY50360-Y50542 and
CC AAY50546-Y50555 represent house dust mite allergen peptide fragments
CC derived from Der p I, Der f II, Der f I and Der f II.
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 20; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 5 DLDA 8
|||||

RESULT 35
AAY39913
ID AAY39913 standard; peptide; 13 AA.
XX
XX AC AAY39913;
XX
XX DT 08-DEC-1999 (first entry)
XX
XX DE Paxillin LD1 peptide.
XX
XX Inhibitor; stereochemically diverse compound production; gene expression;
KW compound library generation; peptidomimetic compound; drug; HIV;
KW cellular proliferation; viral replication; cellular signalling process;
KW catalyst; E6-protein; E6-E6-AP pathway.
XX
XX Synthetic.
XX
XX WO9948897-A2.
XX
XX PD 30-SEP-1999.
```

XX PF 22-MAR-1999; 99WO-US06233.
XX PR 23-MAR-1998; 98US-0079035.
XX PR 22-MAR-1999; 99US-0079035.
XX PA (HARD) HARVARD COLLEGE.
XX XX
XX PI Verdine GL, Chytil M, Didiuk MT, Malinky T;
XX XX WPI; 1999-580411/49.
XX XX
XX PT Generating libraries of stereochemically diverse compounds, especially
XX PT peptidomimetics for use as pharmaceuticals -
XX XX
XX XX Disclosure; Fig 29; 123pp; English.
XX XX
XX CC This sequence represents the paxillin LD1 peptide, and was used to test
XX CC compounds generated by the method of the invention, that were thought to
XX CC be inhibitors of the B6-E6-AP pathway. The method is for generating a
XX CC library of compounds having stereochemical diversity involves selecting
XX CC desired synthetic precursors having a defined stereochemical
XX CC relationship, reacting the synthetic precursors to give a compound having
XX CC a specific stereochemistry and repeating the steps of selecting and
XX CC reacting until the desired library is obtained. The method is useful for
XX CC generating a library of peptidomimetic compounds having stereochemical
XX CC diversity. The compounds may be useful as drugs, e.g. for control of HIV
XX CC production, cellular proliferation, viral replication, gene expression or
XX CC any other cellular signalling process. The compounds may be useful as
XX CC catalysts, either as a ligand for a transition metal capable of mimicking
XX CC a biological environment or by acting with a transition metal catalyst to
XX CC effect a desired enantioselective chemical reaction. The compounds may
XX CC further be useful for generating biomaterials.
XX XX
XX SQ Sequence 13 AA;
XX
XX Query Match 100.0%; Score 20; DB 20; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDA 4
XX ||||
XX Db 1 DLDA 4
XX
XX
XX RESULT 36
XX ID AAB46889 standard; peptide; 13 AA.
XX AC AAB46889;
XX XX
XX DT 09-MAY-2001 (first entry)
XX XX
XX DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #21.
XX XX
XX KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
XX KW cystostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
XX KW vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;
XX KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;
XX KW neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
XX KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
XX KW osteoporosis; inflammation; infection; psoriasis; wound healing.
XX OS Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 5 /note= "D-form residue"
XX FT
XX XX
XX XX DE19933173-A1.
XX XX
XX PD 18-JAN-2001.
XX XX

PF 15-JUL-1999; 99DE-1033173.
XX XX
PR 15-JUL-1999; 99DE-1033173.
XX XX
PA (MERE) MERCK PATENT GMBH.
XX XX
XX PI Joneczyk A, Diefenbach B, Goodman S;
XX XX WPI; 2001-192448/20.
XX XX
XX PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
XX PT useful e.g. for treating thrombosis, coronary heart disease, tumors,
XX PT osteoporosis, inflammation or infections -
XX XX
XX PS Example 1; Page 11; 20pp; German.
XX XX
XX CC This invention describes novel cyclic peptides (I), containing 8 amino
XX CC acid residues and optionally further alpha.omega-aminocarboxylic acid
XX CC residues. Cyclic peptides of formula Cyclo-(Arg-X₁-X₂-X₃-X₄-
XX CC X₅-X₆-R₁) (I) and their salts and solvates. X₁ = Ser, Gly or Thr;
XX CC X₂ = Leu, Ile, Nle, Val or Phe; X₃ = Asp, Glu, Lys or Phe; X₄ =
XX CC Gly, Ala or Ser; X₅ = Leu, Ile, Nle, Val or Phe; X₆ = Arg, Har or
XX CC Lys; R₁ = one or more omega-aminocarboxylic acid residues, having a
XX CC length of 50-2500 mum; or is absent; the amino acid residues are
XX CC optionally derivatized and include D- as well as L-forms (in the case of
XX CC optically active aminoacids). The products of the invention have
XX CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
XX CC antiinflammatory, antibacterial, antipsoriatic, vulnary,
XX CC cerebroprotective, antianginal, antidiabetic, ophthalmological,
XX CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,
XX CC neuroprotective. (I) are used for treating diseases involving expression
XX CC and pathological function of alpha_vbeta_6-integrin receptors, especially
XX CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
XX CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
XX CC wound healing deficiency. Other disclosed disorders to be treated include
XX CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
XX CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
XX CC rubrotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
XX CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
XX CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
XX CC also be useful in analytical biology and molecular biology; e.g.
XX CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
XX CC used to prepare affinity chromatography columns for purifying integrins.
XX CC DNA encoding (I) may be used for treating the same disorders as (I)
XX CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
XX CC receptor inhibiting activity.
XX XX
XX SQ Sequence 13 AA;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DLDA 4
XX ||||
XX Db 3 DLDA 6
XX
XX
XX RESULT 37
XX AAU19089
XX ID AAU19089 standard; Peptide; 13 AA.
XX XX
XX AC AAU19089;
XX XX
XX XX 04-DEC-2001 (first entry)
XX XX
XX XX T-cell epitope containing peptide DPI-26.3.
XX XX
XX KW House dust mite; allergenic peptide; Der p I; Der p II; Der f I;
XX KW Der f II; antiallergenic; immunostimulant; house dust mite allergy;
XX KW T-cell epitope.
XX XX
XX OS Dermatophagoides pteronyssinus.

XX US6268491-B1.
XX 31-JUL-2001.
XX
XX 07-JUN-1995; 95US-0484296.
XX
XX 19-MAY-1995; 95US-0445307.
XX 16-OCT-1991; 91US-0777859.
XX 08-MAY-1992; 92US-0881396.
XX 14-APR-1993; 93WO-US03471.
XX 14-APR-1994; 94US-0227772.
XX (IMMU-) IMMULOGIC PHARM CORP.
XX Garman RD, Greenstein JL, Kuo M, Rogers BL, Franzen HM, Chen X;
XX Evans S, Shaked Z;
XX WPI; 2001-549074/61.
XX Peptides comprising T cell groups of the major allergens from
XX Dermatophagoides (house dust mites), useful for treating house dust
XX mite allergy in humans, and for diagnosing sensitivity to house dust
XX mite protein allergens -
XX Claim 2; Figure 29; 158pp; English.
XX
XX The invention relates to an isolated peptide of the major protein
XX allergens of the genus Dermatophagoides, which comprises at least one T
XX cell group of a protein allergen from Der p (DP) I, DP II, Der f (DF) I
XX or DF II. The isolated peptide comprises at least two regions,
XX each region comprising at least one T cell group of a protein allergen
XX of the genus Dermatophagoides. The regions are derived from the same or
XX different protein allergens of the genus Dermatophagoides. The peptides
XX are useful for treating house dust mite allergy in humans. The peptides
XX are also useful for detecting or diagnosing sensitivity to house dust
XX mite protein allergens. The present peptides have similar or enhanced
XX therapeutic properties as the naturally-occurring allergen, but have
XX reduced side effects, and increased solubility and stability. The
XX present sequence represents an allergenic T-cell epitope containing
XX peptide derived from the Dermatophagoides allergenic proteins.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DLDA 4
XX Db 5 DLDA 8
XX
XX
XX RESULT 38
XX AA09069
XX ID AA09069 standard; peptide; 14 AA.
XX
XX AC AA09069;
XX
XX DT 06-JUL-1999 (first entry)
XX
XX DE E6 binding domain paxillin LD1.
XX
XX KW HPV; E6 transforming protein; E6bp; E6 binding peptide; HPV infection;
XX cervical cancer; E6AP; cellular factor; papillomavirus.
XX
XX OS Unidentified.
XX
XX WO9917616-A1.
XX
XX 15-APR-1999.
XX
XX 06-OCT-1998; 98WO-US20991.

XX 07-OCT-1997; 97US-0061295.
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Androphy EJ, Baleja JD, Chen JJ;
XX WPI; 1999-263855/22.
XX
XX New method to identify candidate compounds which have the ability to
XX interact with a HPV E6 transforming protein
XX
XX Disclosure; Fig 4; 50pp; English.
XX
XX The invention provides a method of evaluation of a candidate compound for
XX the ability to interact with a HPV E6 transforming protein. The method
XX comprises: (a) supplying a three-dimensional (3-D) structure for E6bp;
XX (b) supplying a 3-D structure for the candidate compound; and (c)
XX comparing the 3-D structure of the candidate compound to that of E6bp,
XX where similarity in the structures is indicative of the ability of the
XX candidate compound to interact with the HPV E6 transforming protein. The
XX methods can be used to identify compounds which can be used to treat HPV
XX infections, e.g. a HPV induced cancer such as cervical cancer. The
XX methods of the invention allow rapid and efficient design and evaluation
XX of compound for inhibiting infection by papillomavirus. The present
XX sequence represents a E6 binding domain that can bind to the E6
XX transforming protein.
XX
XX Sequence 14 AA;
XX
XX Query Match 100.0%; Score 20; DB 20; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DLDA 4
XX Db 3 DLDA 6
XX
XX
XX RESULT 39
XX AAB46886
XX ID AAB46886 standard; peptide; 14 AA.
XX
XX AC AAB46886;
XX
XX DT 09-MAY-2001 (first entry)
XX
XX DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #18.
XX
XX KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;
XX cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;
XX vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;
XX ophthalmological; antiarthritic; antirheumatic; antilucer; vasotropic;
XX neuroprotective; alpha_vbeta_6-integrin receptor; thrombosis; tumor;
XX cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;
XX osteoporosis; inflammation; infection; psoriasis; wound healing.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 5 /note= "D-form residue"
XX
XX DE19933173-A1.
XX
XX 18-JAN-2001.
XX
XX 15-JUL-1999; 99DE-1033173.
XX
XX 15-JUL-1999; 99DE-1033173.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX

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PI Jonczyk A, Diefenbach B, Goodman S;
XX WPI; 2001-192448/20.
XX
XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors
PT useful e.g. for treating thrombosis, coronary heart disease, tumors,
PT osteoporosis, inflammation or infections -
XX
XX Example 1; Page 10; 20pp; German.
XX
XX This invention describes novel cyclic peptides (I), containing 8 amino
CC acid residues and optionally further alpha,omega-aminocarboxylic acid
CC residues. Cyclic peptides of formula Cyclo-(Arg-X1-X2-X3-X4-
CC X5-X6-R1) (I) and their salts and solvates. X1 = Ser, Gly or Thr;
CC X2 = Leu, Ile, Nle, Val or Phe; X3 = Asp, Glu, Lys or Phe; X4 =
CC Gly, Ala or Ser; X5 = Leu, Ile, Nle, Val or Phe; X6 = Arg, Har or
CC Lys; R1 = one or more omega-aminocarboxylic acid residues, having a
CC length of 50-2500 mum; or is absent; the amino acid residues are
CC optionally derivatized and include D- as well as L-forms (in the case of
CC optically active aminoacids). The products of the invention have
CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,
CC antiinflammatory, antibacterial, antipsoriatic, vulnerary,
CC cerebroprotective, antianginal, antidiabetic, ophthalmological,
CC antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic,
CC neuroprotective (I) are used for treating diseases involving expression
CC and pathological function of alpha_vbeta_6-integrin receptors, especially
CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,
CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and
CC wound healing deficiency. Other disclosed disorders to be treated include
CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic
CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or
CC rubecotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,
CC acute renal failure, renal inflammation or multiple sclerosis. (I) may
CC also be useful in analytical biology and molecular biology; e.g.
CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be
CC used to prepare affinity chromatography columns for purifying integrins.
CC DNA encoding (I) may be used for treating the same disorders as (I)
CC itself. (I) are well tolerated and have good alpha_vbeta_6-integrin
XX receptor inhibiting activity.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 20; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 3 DLDA 6
|||||
RESULT 40
AAAR73948
ID AAR73948 standard; Peptide; 15 AA.
XX
AC AAR73948;
XX
XX 04-DEC-1995 (first entry)
XX
XX Fragment of T.sergenti 33 kDa protein.
XX
XX bovine small piroplasma protozoa; 33 kDa protein; vaccine;
XX immunogen.
XX
XX Theileria sergenti.
XX
XX AU9470373-A.
XX
XX 09-MAR-1995.
XX
XX 22-AUG-1994; 94AU-0070373.
XX
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```
PR 30-AUG-1993; 93JP-0238864.
XX (NORQ ) NAT INST ANIMAL HEALTH.
XX (KAGA ) CEMO SERO THERAPEUTIC RES INST.
XX Fujisaki K, Kamio T, Kashiwazaki M, Kawazu S, Miyahara T;
XX Nonaka F, Sakai E, Taneno A, Yamada S;
XX WPI; 1995-147719/20.
XX
XX New bovine small piroplasma protozoa peptide(s) - contg. the
XX Lys-Glu-Lys sequence, used for preventing infection or detecting
XX antibodies.
XX Claim 2; Page 16; 20pp; English.
XX
XX This sequence represents a fragment of the principal 33 kDa protein of
XX T.sergenti (see also R73947). T.sergenti is a bovine small piroplasma
XX protozoa. This sequence contains the KEK sequence which is the smallest
XX immunogenic unit of the 33 kDa protein. This protein can be used in a
XX vaccine for prevention of bovine small piroplasma disease.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 20; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 12 DLDA 15
|||||
RESULT 41
AAW04908
ID AAW04908 standard; Protein; 15 AA.
XX
AC AAW04908;
XX
XX 22-DEC-1996 (first entry)
XX
XX N. meningitidis 608B peptide CS-853.
XX
XX Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX Synthetic.
XX
XX WO9629412-A1.
XX
XX 26-SEP-1996.
XX
XX 15-MAR-1996; 96WO-CA00157.
XX
XX 04-AUG-1995; 95US-0001983.
XX 17-MAR-1995; 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
XX
XX Brodeur BR, Hamel J, Martin D, Rioux C;
XX WPI; 1996-443187/44.
XX
XX Neisseria meningitidis antigen, highly conserved between different
XX strains - useful for prodn. of antibodies for immunisation against,
XX or diagnosis of, N. meningitidis infection
XX Claim 24; Page 82; 117pp; English.
XX
XX Example 9 describes the epitope mapping of the 22 kD
XX N. meningitidis protein. Identification was accomplished
XX using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
```

SQ Sequence 15 AA;

Query Match 100.0%; Score 20; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
 Db 12 DLDA 15

RESULT 42

AAW04909
 ID AAW04909 standard; Protein; 15 AA.

XX AC AAW04909;

DT 22-DEC-1996 (first entry)

DE N. meningitidis 608B peptide CS-854.

KW Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

XX OS Synthetic.

XX PN WO9629412-A1.

XX PD 26-SEP-1996.

XX PF 15-MAR-1996; 96WO-CA00157.

XX PR 04-AUG-1995; 95US-0001983.

XX PR 17-MAR-1995; 95US-0406362.

XX PA (IAFB-) IAF BIO VAC INC.

XX PI Brodeur BR, Hamel J, Martin D, Rioux C;

XX DR WPI; 1996-443187/44.

XX PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection

XX PS Claim 24; Page 83; 117pp; English.

XX CC Example 9 describes the epitope mapping of the 22 kD

CC N. meningitidis protein. Identification was accomplished

CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 20; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
 Db 2 DLDA 5

RESULT 43

AAG64814
 ID AAG64814 standard; Peptide; 15 AA.

XX AC AAG64814;

DT 19-SEP-2001 (first entry)

XX DE Cytokine-like peptide screening method related peptide #14.
 XX Cytokine-like peptide; peptide mimic; viral disease.

XX OS Unidentified.

XX PN WO200148478-A1.

XX PD 05-JUL-2001.

XX PF 27-DEC-2000; 2000WO-JP09278.

XX PR 27-DEC-1999; 99JP-0369990.

XX PA (TORA) TORAY IND INC.

XX PI Sato A, Sone S;

XX DR WPI; 2001-418329/44.

XX PT Cytokine-like peptides screened by binding activity with antibody
 PT having activity of neutralising cytokine, capable of expressing
 PT biological activity of cytokine, useful as low-molecular peptide mimics
 PT for treating e.g. viral diseases -

XX PS Example 10; Fig 7; 33pp; Japanese.

XX CC The present invention describes a method of screening a cytokine-like
 CC peptide, comprising searching for a peptide, which is capable of
 CC expressing the biological activity of the cytokine, by binding to an
 CC antibody which has an activity of neutralising a cytokine, from amongst
 CC peptides not having been confirmed as being with the biological activity
 CC of the cytokine. The peptides identified using the method are applicable
 CC as low-molecular peptide mimics of cytokine for treating e.g. viral
 CC diseases.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 20; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
 Db 11 DLDA 14

RESULT 44

ABB44423
 ID ABB44423 standard; Peptide; 18 AA.

XX AC ABB44423;

XX DT 04-FEB-2002 (first entry)

XX DE Peptide #11929 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00669.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human fetal liver -
 XX
 XX Claim 27; SEQ ID NO 37058; 639pp + sequence listing; English.
 XX The invention relates to a single exon nucleic acid probe for
 XX measuring human gene expression in a sample derived from human foetal
 XX liver. The single exon nucleic acid probes may be used for predicting,
 XX measuring and displaying gene expression in samples derived from human
 XX fetal liver. The present sequence is a peptide encoded by a single exon
 XX nucleic acid probe of the invention.
 XX Note: The sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 18 AA;
 CC
 CC Query Match 100.0%; Score 20; DB 22; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 3 DLDA 6
 IIII
 RESULT 45
 ABB27270
 ID ABB27270 standard; Protein; 18 AA.
 XX
 XX AC ABB27270;
 XX
 XX 23-JAN-2002 (first entry)
 XX
 XX Protein #9269 encoded by probe for measuring heart cell gene expression.
 XX Human; gene expression; heart; microarray; vascular system;
 XX cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease.
 XX Homo sapiens.
 XX
 XX WO200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00666.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts -
 XX
 XX Claim 15; SEQ ID NO 29040; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 18 AA;
 CC
 CC Query Match 100.0%; Score 20; DB 22; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 3 DLDA 6
 IIII

Search completed: February 6, 2003, 11:19:36
 Job time : 28.8333 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 ; Search time 9.33333 Seconds
(without alignments)
12.610 Million cell updates/sec

Title: PAT943-2
Perfect score: 20
Sequence: 1 dlda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	6	2	US-08-763-302-2
2	20	100.0	6	4	US-09-177-595-2
3	20	100.0	8	2	US-08-568-310D-3
4	20	100.0	8	4	US-08-817-811-4
5	20	100.0	8	4	US-08-817-811-5
6	20	100.0	8	4	US-09-270-455-3
7	20	100.0	12	4	US-08-817-811-9
8	20	100.0	12	4	US-08-817-811-23
9	20	100.0	12	4	US-08-817-811-24
10	20	100.0	12	4	US-08-817-811-25
11	20	100.0	12	4	US-08-817-811-29
12	20	100.0	13	2	US-08-482-142-135
13	20	100.0	13	2	US-08-478-572-135
14	20	100.0	13	4	US-08-484-296-135
15	20	100.0	15	4	US-08-913-362-22
16	20	100.0	15	4	US-08-913-362-23
17	20	100.0	18	4	US-08-477-928A-24
18	20	100.0	20	1	US-08-171-299B-16
19	20	100.0	20	4	US-08-817-811-1
20	20	100.0	20	4	US-08-817-811-37
21	20	100.0	24	4	US-09-314-242-9
22	20	100.0	26	1	US-08-057-161-2
23	20	100.0	26	2	US-08-482-142-21
24	20	100.0	26	2	US-08-482-142-22
25	20	100.0	26	2	US-08-482-142-37
26	20	100.0	26	2	US-08-482-142-134
27	20	100.0	26	2	US-08-482-142-168

Sequence 21, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 134, App
Sequence 168, App
Sequence 4, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 134, App
Sequence 168, App
Sequence 4, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 134, App
Sequence 168, App
Sequence 12, Appl
Sequence 13, Appl
Sequence 30, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-763-302-2
; Sequence 2, Application US/08763302
; Patent No. 5932692
; GENERAL INFORMATION:
; APPLICANT: FASSINA, GIORGIO
; APPLICANT: VERDOLIVA, ANTONIO
; APPLICANT: RUVO, MENOTTI
; TITLE OF INVENTION: ANTIGENIC PEPTIDES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763.302
; FILING DATE: 10-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT MI95A002582
; FILING DATE: 11-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2149-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-763-302-2

Query Match 100.0%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

Db 2 DLDA 5
||||

RESULT 2

US-09-177-595-2
; Sequence 2, Application US/09177595
; Patent No. 6222011
; GENERAL INFORMATION:
; APPLICANT: FASSINA, GIORGIO
; APPLICANT: VERDOLIVA, ANTONIO
; APPLICANT: ROVO, MEMOTTI
; TITLE OF INVENTION: ANTIGENIC PEPTIDES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/177,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/763,302
; FILING DATE: 10-DEC-1996
; APPLICATION NUMBER: IT MI95A002582
; FILING DATE: 11-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B. J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2149-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-177-595-2

Query Match 100.0%; Score 20; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||

Db 2 DLDA 5

RESULT 3

US-08-568-310D-3
; Sequence 3, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER, & O'ROURKE

; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 3:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 8
US-08-568-310D-3

Query Match 100.0%; Score 20; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||

Db 4 DLDA 7

RESULT 4

US-08-817-811-4
; Sequence 4, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-817-811-4

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 4 DLDA 7

RESULT 5
US-08-817-811-5
Sequence 5, Application US/08817811
Patent No. 6174528
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relif, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-817-811-5

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 2 DLDA 5

RESULT 6
US-09-270-455-3
Sequence 3, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 8
US-09-270-455-3

Query Match 100.0%; Score 20; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 4 DLDA 7

RESULT 7
US-08-817-811-9
Sequence 9, Application US/08817811
Patent No. 6174528
GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-817-811-9
Query Match 100.0%; Score 20; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 4 DLDA 7
RESULT 8
US-08-817-811-23
Sequence 23, Application US/08817811
Patent No. 6174528
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-817-811-23
Query Match 100.0%; Score 20; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 4 DLDA 7
RESULT 9
US-08-817-811-24
Sequence 24, Application US/08817811
Patent No. 6174528
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-24

Query Match 100.0%; Score 20; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 3 DLDA 6

RESULT 10
US-08-817-811-25
; Sequence 25, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-25

Query Match 100.0%; Score 20; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 2 DLDA 5

RESULT 11
US-08-817-811-29
; Sequence 29, Application US/08817811
; Patent No. 6174528

;
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-29

Query Match 100.0%; Score 20; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 1 DLDA 4

RESULT 12
US-08-482-142-135
; Sequence 135, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA

FRAGMENT TYPE: internal
US-08-484-296-135

Query Match 100.0%; Score 20; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 5 DLDA 8

RESULT 15

US-08-913-362-22
; Sequence 22, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
US-08-913-362-22

Query Match 100.0%; Score 20; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 12 DLDA 15

RESULT 16

US-08-913-362-23
; Sequence 23, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
US-08-913-362-23

Query Match 100.0%; Score 20; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 2 DLDA 5

RESULT 17

US-08-477-928A-24
; Sequence 24, Application US/08477928A
; Patent No. 6207389
; GENERAL INFORMATION:
; APPLICANT: Dosch, Hans M.
; TITLE OF INVENTION: METHODS FOR CONTROLLING T
; TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS
; STREET: 1299 Pennsylvania Avenue

; CITY: Washington D.C.
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,928A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36902
; REFERENCE/DOCKET NUMBER: 19060-0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 639 7700
; TELEFAX: (202) 639 7890
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-928A-24

Query Match 100.0%; Score 20; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 8 DLDA 11

RESULT 18
US-08-171-299B-16
; Sequence 16, Application US/08171299B
; Patent No. 5599665
; GENERAL INFORMATION:
; APPLICANT: Barbieri, Joseph T.
; APPLICANT: Frank, Dara W.
; TITLE OF INVENTION: EXOENZYME S' PROTEIN PREPARATION AND CLONED EXOENZYME S
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,299B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.90871
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-171-299B-16
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 2 DLDA 5

RESULT 19
US-08-817-811-1
; Sequence 1, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-817-811-1

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 4 DLDA 7

RESULT 20
US-08-817-811-37
; Sequence 37, Application US/08817811

Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-37

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 14 DLDA 17

RESULT 21
US-09-314-242-9
; Sequence 9, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
; FILE REFERENCE: 5556.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
; FEATURE:
; OTHER INFORMATION: Xaa = The amino acid residue was not determinable.

US-09-314-242-9

Query Match 100.0%; Score 20; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 8 DLDA 11

RESULT 22
US-08-057-161-2
; Sequence 2, Application US/08057161
; Patent No. 5371189
; GENERAL INFORMATION:
; APPLICANT: Helderman, J. H.
; TITLE OF INVENTION: MONOCYTE-DERIVED INSULIN RECEPTOR
; TITLE OF INVENTION: REGULATORY FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 133 Carnegie Way, N.W., Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/057,161
; FILING DATE: 19930430
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 2200.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; TISSUE TYPE: Monocyte
; CELL TYPE: P388D1 (ATCC Accession No. 5371189 TIB 63)
US-08-057-161-2

Query Match 100.0%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 16 DLDA 19

RESULT 23
US-08-482-142-21
; Sequence 21, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia

APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-482-142-21

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||
Db 15 DLDA 18

RESULT 24
US-08-482-142-22
Sequence 22, Application US/08482142,
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM

STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-482-142-22

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||
Db 3 DLDA 6

RESULT 25
US-08-482-142-37
Sequence 37, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-482-142-37

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 6 DLDA 9

RESULT 26
US-08-482-142-134
Sequence 134, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-482-142-134

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 6 DLDA 9

RESULT 27
US-08-482-142-168
Sequence 168, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-482-142-168

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 6 DLDA 9

RESULT 28

US-08-478-572-21
; Sequence 21, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-478-572-21

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
| | | |
Db 15 DLDA 18

RESULT 29

US-08-478-572-22
; Sequence 22, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-478-572-22

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
| | | |
Db 3 DLDA 6

RESULT 30

US-08-478-572-37
; Sequence 37, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; US-08-478-572-37

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 6 DLDA 9

RESULT 31
US-08-478-572-134
; Sequence 134, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-478-572-168

; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-478-572-134

Query Match 100.0%; Score 20; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 6 DLDA 9

RESULT 32
US-08-478-572-168
; Sequence 168, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.605
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-478-572-168

ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.60S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-484-296-22

Query Match 100.0%; Score 20; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 3 DLDA 6

RESULT 36
US-08-484-296-37
Sequence 37, Application US/08484296
Patent No. 6268491
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995

ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.60S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-484-296-37

Query Match 100.0%; Score 20; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 6 DLDA 9

RESULT 37
US-08-484-296-134
Sequence 134, Application US/08484296
Patent No. 6268491
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.60S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-484-296-134
; FRAGMENT TYPE: internal

Query Match 100.0%; Score 20; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 6 DLDA 9

RESULT 38

US-08-484-296-168
; Sequence 168, Application US/08484296
; Patent No. 6268491

GENERAL INFORMATION:

APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mel-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995

ATTORNEY/AGENT INFORMATION:

NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976

REFERENCE/DOCKET NUMBER: 017.6US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 466-6000

TELEFAX: (617) 466-6040

INFORMATION FOR SEQ ID NO: 168:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-484-296-168

Query Match 100.0%; Score 20; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 6 DLDA 9

RESULT 39

PCT-US95-04481-12
; Sequence 12, Application PC/TUS9504481
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dus:

NUMBER OF SEQUENCES: 54

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04481

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/227,772

FILING DATE: April 14, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Vanstone, Darlene A.

REGISTRATION NUMBER: 35,279

REFERENCE/DOCKET NUMBER: 017.5 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 466-6000

TELEFAX: (617) 466-6040

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

PCT-US95-04481-12

Query Match 100.0%; Score 20; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 15 DLDA 18

RESULT 40

PCT-US95-04481-13

; Sequence 13, Application PC/TUS9504481

; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dust

NUMBER OF SEQUENCES: 54

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04481

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/227,772

FILING DATE: April 14, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Vanstone, Darlene A.

REGISTRATION NUMBER: 35,279

REFERENCE/DOCKET NUMBER: 017.5 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 466-6000

TELEFAX: (617) 466-6040

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04481-13

Query Match 100.0%; Score 20; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 3 DLDA 6

RESULT 41
PCT-US95-04481-30
; Sequence 30, Application PC/TUS9504481
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dust Mit
; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04481
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,772
; FILING DATE: April 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 017.5 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04481-30

Query Match 100.0%; Score 20; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 6 DLDA 9

RESULT 42
US-08-141-324-12
; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; PROTEASE

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-12

Query Match 100.0%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 7 DLDA 10

RESULT 43
US-08-541-902-12
; Sequence 12, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; PROTEASE
; NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/141,324
;; FILING DATE: 21-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferber, Donna M.
;; REGISTRATION NUMBER: 33,878
;; REFERENCE/DOCKET NUMBER: 44-93
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 303-499-8080
;; TELEFAX: 303-499-8089
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-541-902-12

Query Match 100.0%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 7 DLDA 10

RESULT 44
US-08-817-811-13
; Sequence 13, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:

;; TOPOLOGY: linear
US-08-817-811-13

Query Match 100.0%; Score 20; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 12 DLDA 15

RESULT 45
US-08-817-811-14
; Sequence 14, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-14

Query Match 100.0%; Score 20; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

Search completed: February 6, 2003, 11:24:04
Job time : 10.3333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:22:09 ; Search time 5.83333 Seconds
(without alignments)
15.202 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 419

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	18	10	US-09-299-473A-2
3	20	100.0	20	9	US-10-044-034-22
4	20	100.0	26	10	US-09-740-516-4
5	20	100.0	33	10	US-09-746-919-38
6	20	100.0	40	12	US-10-025-167-45
7	20	100.0	50	9	US-09-932-172A-2
8	20	100.0	50	9	US-09-955-581-2
9	20	100.0	50	9	US-10-039-119A-2
10	20	100.0	50	10	US-09-864-761-39240
11	20	100.0	50	10	US-09-299-473A-1
12	20	100.0	52	10	US-09-864-761-39301
13	20	100.0	58	10	US-09-864-761-43108
14	20	100.0	62	9	US-09-738-626-5087
15	20	100.0	63	9	US-09-738-626-4594
16	20	100.0	63	10	US-09-867-550-466
17	20	100.0	65	10	US-09-864-761-42283
18	20	100.0	65	10	US-09-864-761-43617
19	20	100.0	74	10	US-09-815-242-13358

20	20	100.0	77	10	US-09-815-242-13674
21	20	100.0	81	10	US-09-867-550-320
22	20	100.0	89	9	US-09-738-626-5626
23	20	100.0	89	10	US-09-819-930-2
24	20	100.0	89	10	US-09-819-930-4
25	20	100.0	89	10	US-09-755-187-2
26	20	100.0	90	10	US-09-826-589-3
27	20	100.0	90	10	US-09-826-589-4
28	20	100.0	90	10	US-09-872-185B-11
29	20	100.0	90	10	US-09-872-185B-12
30	20	100.0	94	10	US-09-864-761-48068
31	20	100.0	95	9	US-09-981-353-98
32	20	100.0	95	10	US-09-746-919-24
33	20	100.0	95	10	US-09-956-425-18
34	20	100.0	95	10	US-09-956-425-21
35	20	100.0	95	10	US-09-956-425-22
36	20	100.0	95	10	US-09-956-425-23
37	20	100.0	95	10	US-09-919-172-102
38	20	100.0	97	10	US-09-746-919-28
39	20	100.0	98	10	US-09-915-582-51
40	20	100.0	98	10	US-09-915-582-67
41	20	100.0	99	10	US-09-746-919-22
42	20	100.0	101	9	US-09-738-626-3769
43	20	100.0	102	10	US-09-746-919-26
44	20	100.0	109	12	US-10-062-254-76
45	20	100.0	117	9	US-09-906-209-6

ALIGNMENTS

RESULT 1

- US-09-864-761-42568
- ; Sequence 42568, Application US/09864761
- ; Patent No. US20020048763A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Penn, Sharon G.
- ; APPLICANT: Rank, David R.
- ; APPLICANT: Hanzel, David K.
- ; APPLICANT: Chen, Wensheng
- ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
- ; FILE REFERENCE: Aemlica-X-1
- ; CURRENT APPLICATION NUMBER: US/09/864,761
- ; CURRENT FILING DATE: 2001-05-23
- ; PRIOR APPLICATION NUMBER: US 60/180,312
- ; PRIOR FILING DATE: 2000-02-04
- ; PRIOR APPLICATION NUMBER: US 60/207,456
- ; PRIOR FILING DATE: 2000-05-26
- ; PRIOR APPLICATION NUMBER: US 09/632,366
- ; PRIOR FILING DATE: 2000-08-03
- ; PRIOR APPLICATION NUMBER: GB 24263.6
- ; PRIOR FILING DATE: 2000-10-04
- ; PRIOR APPLICATION NUMBER: US 60/236,359
- ; PRIOR FILING DATE: 2000-09-27
- ; PRIOR APPLICATION NUMBER: PCT/US01/00666
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00667
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00664
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00669
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00665
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00668
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00663
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00662
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00661
- ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42568
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133246.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EST_HUMAN HIT: A0117241.1, EVALUATE 2.50e-01
US-09-864-761-42568

Query Match 100.0%; Score 20; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 3 DLDA 6

RESULT 2

US-09-299-473A-2
; Sequence 2, Application US/09299473A
; Patent No. US20020099008A1
; GENERAL INFORMATION:
; APPLICANT: Twardzik, Daniel R
; APPLICANT: Felker, Thomas S
; APPLICANT: Stefan, Paskell L
; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR
; TITLE OF INVENTION: STIMULATING STEM CELL PROLIFERATION AND MIGRATION
; FILE REFERENCE: STEMI100
; CURRENT APPLICATION NUMBER: US/09/299,473A
; CURRENT FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-299-473A-2

Query Match 100.0%; Score 20; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 15 DLDA 18

RESULT 3

US-10-044-034-22
; Sequence 22, Application US/10044034
; Patent No. US20020169264A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.

; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FBRC:006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-10-044-034-22

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 4 DLDA 7

RESULT 4

US-09-740-516-4
; Sequence 4, Application US/09740516
; Patent No. US20010011124A1
; GENERAL INFORMATION:
; APPLICANT: HU, ERDING
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A HUMAN 7-TM RECEPTOR SIMILAR TO MURINE
; TITLE OF INVENTION: FRIZZLED-6 GENE
; FILE REFERENCE: GH-70060-DIC1
; CURRENT APPLICATION NUMBER: US/09/740,516
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 08/987,289
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 09/304,485
; PRIOR FILING DATE: 1999-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-740-516-4

Query Match 100.0%; Score 20; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 19 DLDA 22

RESULT 5

US-09-746-919-38
; Sequence 38, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/746,919
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/045,467
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Behlinger, Peter J.
REGISTRATION NUMBER: 28,906
REFERENCE/DOCKET NUMBER: 5600-0001.36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:33
US-09-746-919-38

Query Match 100.0%; Score 20; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 6 DLDA 9

RESULT 6
US-10-025-167-45
Sequence 45, Application US/10025167
Patent No. US20020127693A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA A.
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
HAYDEN, MARK
KLASS, MICHAEL R.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.

STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,167
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/049,698
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/828,856
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6068.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20020127693A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-025-167-45

Query Match 100.0%; Score 20; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 15 DLDA 18

RESULT 7
US-09-932-172A-2
Sequence 2, Application US/09932172A
Patent No. US20020169119A1
GENERAL INFORMATION:
APPLICANT: STEM CELL PHARMACEUTICALS, INC.
APPLICANT: TWARDZIK, Daniel R.
APPLICANT: PERNET, Andre
APPLICANT: FELKER, Thomas S.
APPLICANT: PASKELL, Stefan
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF
FILE REFERENCE: STEMI110-3
CURRENT APPLICATION NUMBER: US/09/932,172A
CURRENT FILING DATE: 2001-08-17
PRIORITY APPLICATION NUMBER: US 09/641,587
PRIORITY FILING DATE: 2000-08-17
PRIORITY APPLICATION NUMBER: US 09/492,935
PRIORITY FILING DATE: 2000-01-27
PRIORITY APPLICATION NUMBER: US 09/378,567
PRIORITY FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-932-172A-2

Query Match 100.0%; Score 20; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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|
|
|
Db 47 DLDA 50

RESULT 8

US-09-955-581-2
; Sequence 2, Application US/09955581
; Patent No. US20020169131A1
; GENERAL INFORMATION:
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.
; APPLICANT: TWARDZIK, Daniel
; APPLICANT: PASKELL, Stefan
; APPLICANT: FELKER, Thomas
; TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USE
; FILE REFERENCE: STEM1100-3
; CURRENT APPLICATION NUMBER: US/09/955,581
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/559,248
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/299,473
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: US 09/459,813
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-955-581-2

Query Match 100.0%; Score 20; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 47 DLDA 50

RESULT 9

US-10-039-119A-2
; Sequence 2, Application US/10039119A
; Publication No. US20020193301A1
; GENERAL INFORMATION:
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.
; APPLICANT: TWARDZIK, Daniel R.
; APPLICANT: PERNET, Andre
; APPLICANT: FELKER, Thomas S.
; APPLICANT: PASKELL, Stefan
; TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USE
; FILE REFERENCE: STEM110-4
; CURRENT APPLICATION NUMBER: US/10/039,119A
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/641,587
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/492,935
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: US 09/378,567
; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-039-119A-2

Query Match 100.0%; Score 20; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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|
|
Db 47 DLDA 50

RESULT 10

US-09-864-761-39240
; Sequence 39240, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39240
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: MAP TO AC005701.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: P39057, EVALUE 2.00e-04
US-09-864-761-39240

Query Match          100.0%; Score 20; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 32 DLDA 35

RESULT 11
US-09-299-473A-1
; Sequence 1, Application US/09299473A
; Patent No. US20020099008A1
; GENERAL INFORMATION:
; APPLICANT: Twardzik, Daniel R
; APPLICANT: Felker, Thomas S
; APPLICANT: Stefan, Paskell L
; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR
; FILE REFERENCE: STEM1100
; CURRENT APPLICATION NUMBER: US/09/299,473A
; CURRENT FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-299-473A-1

Query Match          100.0%; Score 20; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 47 DLDA 50

RESULT 12
US-09-864-761-39301
; Sequence 39301, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
```

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;
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39301
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005155.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: P29972, EVALUE 2.00e-24
; OTHER INFORMATION: EST_HUMAN HIT: BF477059.1, EVALUE 3.00e-23
US-09-864-761-39301

Query Match          100.0%; Score 20; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 38 DLDA 41

RESULT 13
US-09-864-761-43108
; Sequence 43108, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
```

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43108
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL035416.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P32892, EVALUATE 2.00e+00
US-09-864-761-43108

Query Match 100.0%; Score 20; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 33 DLDA 36

RESULT 14
US-09-738-626-5087
; Sequence 5087, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5087
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5087

Query Match 100.0%; Score 20; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 8 DLDA 11

RESULT 15
US-09-738-626-4594
; Sequence 4594, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4594
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4594

Query Match 100.0%; Score 20; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 27 DLDA 30

RESULT 16
US-09-867-550-466
; Sequence 466, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.

; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206Ae1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-466

Query Match 100.0%; Score 20; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 2 DLDA 5

RESULT 17
US-09-864-761-42283
; Sequence 42283, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42283
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC018720.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
; OTHER INFORMATION: EST HUMAN HIT: BE720191.1, EVALUATE 3.00e-31
; OTHER INFORMATION: SWISSPROT HIT: P53972, EVALUATE 6.00e-02
US-09-864-761-42283

Query Match 100.0%; Score 20; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 6 DLDA 9

RESULT 18
US-09-864-761-43617
; Sequence 43617, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43617
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002036.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
; OTHER INFORMATION: EST_HUMAN HIT: AA434168.1, EVALUATE 2.00e-32
; OTHER INFORMATION: SWISSPROT HIT: P57080, EVALUATE 2.00e-13
US-09-864-761-43617
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Query Match          100.0%; Score 20; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 DLDA 4
    ||||
Db 45 DLDA 48
```

RESULT 19

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US-09-815-242-13358
; Sequence 13358, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 74
```

```
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13358
```

```
Query Match          100.0%; Score 20; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 DLDA 4
    ||||
Db 30 DLDA 33
```

RESULT 20

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US-09-815-242-13674
; Sequence 13674, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13674
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13674
```

```
Query Match          100.0%; Score 20; DB 10; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DLDA 4
    ||||
Db 33 DLDA 36
```

RESULT 21

```
US-09-867-550-320
; Sequence 320, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells
```

; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-320

Query Match 100.0%; Score 20; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 1 DLDA 4

RESULT 22
US-09-738-626-5626
; Sequence 5626, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5626
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5626

Query Match 100.0%; Score 20; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 85 DLDA 88

RESULT 23
US-09-819-930-2
; Sequence 2, Application US/09819930
; Patent No. US20020090700A1
; GENERAL INFORMATION:
; APPLICANT: FARWICK, MIKE
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING THE PTSH GENE
; FILE REFERENCE: MAS/21123/278412
; CURRENT APPLICATION NUMBER: US/09/819,930
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/755,187
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: DE 100 01 101.2
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-819-930-2

Query Match 100.0%; Score 20; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 85 DLDA 88

RESULT 24
US-09-819-930-4
; Sequence 4, Application US/09819930
; Patent No. US20020090700A1
; GENERAL INFORMATION:
; APPLICANT: FARWICK, MIKE
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING THE PTSH GENE
; FILE REFERENCE: MAS/21123/278412
; CURRENT APPLICATION NUMBER: US/09/819,930
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/755,187
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: DE 100 01 101.2
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-819-930-4

Query Match 100.0%; Score 20; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 85 DLDA 88

RESULT 25
US-09-755-187-2
; Sequence 2, Application US/09755187
; Patent No. US20020094554A1
; GENERAL INFORMATION:
; APPLICANT: Farwick, Mike
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; TITLE OF INVENTION: New Nucleotide Sequences Encoding the PTSH Gene
; FILE REFERENCE: 21123/275573
; CURRENT APPLICATION NUMBER: US/09/755,187
; CURRENT FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2

; LENGTH: 89
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-755-187-2

Query Match 100.0%; Score 20; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 85 DLDA 88

RESULT 26
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David

; APPLICANT: Schmidt, Ann Marie

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-3

Query Match 100.0%; Score 20; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 59 DLDA 62

RESULT 27
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-4

Query Match 100.0%; Score 20; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 59 DLDA 62

RESULT 28
US-09-872-185B-11
; Sequence 11, Application US/09872185B

; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

Query Match 100.0%; Score 20; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 59 DLDA 62

RESULT 29
US-09-872-185B-12
; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Herold, Kevan

; APPLICANT: Yan, Shi Du

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Lamster, Ira

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION

; FILE REFERENCE: 0575/64080

; CURRENT APPLICATION NUMBER: US/09/872,185B

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-872-185B-12

Query Match 100.0%; Score 20; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 59 DLDA 62

RESULT 30
US-09-864-761-48068
; Sequence 48068, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL

; FILE REFERENCE: Acomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48068
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009594.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EST HUMAN HIT: A1962273.1, EVALUE 5.00e-17
; OTHER INFORMATION: SWISSPROT HIT: Q95155, EVALUE 1.00e-23
; NAME/KEY: unsure
; LOCATION: 8
US-09-864-761-48068

Query Match 100.0%; Score 20; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 48 DLDA 51

RESULT 31
US-09-981-353-98
; Sequence 98, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program

; SEQ ID NO 98
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1422432CD1
US-09-981-353-98

Query Match 100.0%; Score 20; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 60 DLDA 63

RESULT 32
US-09-746-919-24
; Sequence 24, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,919
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,467
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 5600-0001.36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; INDIVIDUAL ISOLATE: Of SEQ ID NO:23 (HuIFNtau7).
US-09-746-919-24

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
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|
|
|
Db 56 DLDA 59

RESULT 33

US-09-956-425-18
; Sequence 18, Application US/09956425;
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-425-18

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 34

US-09-956-425-21
; Sequence 21, Application US/09956425;
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 95
; TYPE: PRT
; ORGANISM: horse
US-09-956-425-21

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 35
US-09-956-425-22
; Sequence 22, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 95
; TYPE: PRT
; ORGANISM: dog
US-09-956-425-22

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 36

US-09-956-425-23
; Sequence 23, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 95
; TYPE: PRT
; ORGANISM: chicken
US-09-956-425-23

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 37

US-09-919-172-102
; Sequence 102, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1422432CD1
US-09-919-172-102

Query Match 100.0%; Score 20; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 60 DLDA 63

RESULT 38
US-09-746-919-28
; Sequence 28, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,919
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,467
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 5600-0001.36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; OTHER INFORMATION: of SEQ ID NO:27 (HuIFNtau5).
US-09-746-919-28

Query Match 100.0%; Score 20; DB 10; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 56 DLDA 59

RESULT 39
US-09-915-582-51
; Sequence 51, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-51

Query Match 100.0%; Score 20; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 73 DLDA 76

RESULT 40
US-09-915-582-67
; Sequence 67, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67

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; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-67

Query Match      100.0%; Score 20; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 73 DLDA 76

RESULT 41
US-09-746-919-22
; Sequence 22, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09746.919
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,467
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 5600-0001.36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence

;
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).
US-09-746-919-22

Query Match      100.0%; Score 20; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 56 DLDA 59

RESULT 42
US-09-738-626-3769
; Sequence 3769, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3769
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3769

Query Match      100.0%; Score 20; DB 9; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

RESULT 43
US-09-746-919-26
; Sequence 26, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,919
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,467
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.

REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 5600-0001.36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0960
TELEFAX: 650-324-0960

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: predicted amino acid coding sequence
INDIVIDUAL ISOLATE: of SEQ ID NO:25 (Huifntaud).

US-09-746-919-26
Query Match 100.0%; Score 20; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 56 DLDA 59

RESULT 44
US-10-062-254-76
Sequence 76, Application US/10062254
Patent No. US20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B

APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Hantke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun

TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/169767
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/172958
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 76

LENGTH: 109
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-062-254-76

Query Match 100.0%; Score 20; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 93 DLDA 96

RESULT 45
US-09-906-209-6
Sequence 6, Application US/09906209
Patent No. US20020165385A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve

APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Ilag, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucumutase Genes

FILE REFERENCE: BB1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000

NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 117

TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: UNSURE

LOCATION: (108)
OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-6

Query Match 100.0%; Score 20; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 1111

Thu Feb 6 12:30:07 2003

Db 83 DLDA 86

Search completed: February 6, 2003, 11:39:43
Job time : 6.83333 secs

pat943-2.rapb

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:59 ; Search time 133.167 Seconds
(without alignments)
19.366 Million cell updates/sec

Title: PAT943-2
Perfect score: 20
Sequence: 1 dlda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 10241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
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- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	7	25	US-10-130-157-226
2	20	100.0	8	9	US-08-568-310C-3
3	20	100.0	9	12	US-08-864-983A-10
4	20	100.0	10	22	US-09-800-187-54
5	20	100.0	11	18	US-09-461-774-20
6	20	100.0	13	6	US-08-227-772-135

7	20	100.0	13	8	US-08-445-307A-135
8	20	100.0	13	16	US-09-373-597-3
9	20	100.0	14	1	PCT-US98-20991-4
10	20	100.0	15	20	US-09-884-883-22
11	20	100.0	15	20	US-09-884-883-23
12	20	100.0	17	8	US-09-437-413-2
13	20	100.0	18	1	PCT-US01-00663-38679
14	20	100.0	18	6	US-08-237-363-24
15	20	100.0	18	22	US-09-299-473A-2
16	20	100.0	18	22	US-09-864-761-42568
17	20	100.0	18	25	US-10-182-993-37608
18	20	100.0	18	25	US-10-182-995-29040
19	20	100.0	18	25	US-10-182-997-26863
20	20	100.0	18	26	US-10-203-134-38471
21	20	100.0	18	26	US-10-203-136-38459
22	20	100.0	18	26	US-10-203-137-38679
23	20	100.0	18	26	US-10-203-139-37058
24	20	100.0	19	19	US-09-512-563-43
25	20	100.0	19	19	US-09-512-563A-43
26	20	100.0	19	19	US-09-512-563C-43
27	20	100.0	20	3	US-07-698-925A-1
28	20	100.0	20	13	US-08-944-147-22
29	20	100.0	20	13	US-08-944-147-22
30	20	100.0	20	24	US-10-044-034-22
31	20	100.0	21	3	US-07-946-304-2
32	20	100.0	22	3	US-07-969-314A-10
33	20	100.0	24	14	US-09-080-428-9
34	20	100.0	25	21	US-09-724-059-530377
35	20	100.0	25	21	US-09-724-059-530378
36	20	100.0	25	21	US-09-724-059-530379
37	20	100.0	25	21	US-09-724-059-53338
38	20	100.0	25	21	US-09-724-059-538495
39	20	100.0	25	21	US-09-724-059-538496
40	20	100.0	25	21	US-09-724-059-559241
41	20	100.0	25	21	US-09-724-059-559242
42	20	100.0	25	21	US-09-724-059-559243
43	20	100.0	25	21	US-09-724-059-559244
44	20	100.0	25	21	US-09-724-059-559245
45	20	100.0	25	21	US-09-724-059-559246

ALIGNMENTS

RESULT 1
US-10-130-157-226
; Sequence 226, Application US/10130157
; GENERAL INFORMATION:
; APPLICANT: GENEART GmbH
; TITLE OF INVENTION: The Genome of the HIV-1 Inter-Subtype (C/B') and Use Thereof
; FILE REFERENCE: WAG-001 PCT
; CURRENT APPLICATION NUMBER: US/10/130.157
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: DE 19955089.1
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 226
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-130-157-226

Query Match 100.0%; Score 20; DB 25; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 2 DLDA 5

RESULT 2

US-08-568-310C-3
; Sequence 3, Application US/08568310C.
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MELLER AND ASSOCIATES
; STREET: 50 EAST 42nd STREET
; STREET: 19th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568-310C
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: Klein, Milton
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 3:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 8
US-08-568-310C-3
Query Match 100.0%; Score 20; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 4 DLDA 7
RESULT 3
US-08-864-983A-10
; Sequence 10, Application US/08864983A
; GENERAL INFORMATION:
; APPLICANT: Kawauchi, Yasushi
; APPLICANT: Takasaki, Jun
; APPLICANT: Yasunaga, Tomoe
; APPLICANT: Masuhiko
; TITLE OF INVENTION: NOVEL MONOCLONAL ANTIBODY HAVING
; TITLE OF INVENTION: INHIBITORY ACTIVITY AGAINST TYPE II PHOSPHOLIPASE A2 AND
; TITLE OF INVENTION: PROTEIN COMPRISING A PART THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,983A
FILING DATE: 29-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02714
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI 6-340006
FILING DATE: 29-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: O-45511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL LINE: 1.4
US-08-864-983A-10
Query Match 100.0%; Score 20; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 1 DLDA 4
RESULT 4
US-09-800-187-54
; Sequence 54, Application US/09800187
; GENERAL INFORMATION:
; APPLICANT: GROZINGER, CHRISTINA M.
; APPLICANT: HASSIG, CHRISTIAN A.
; APPLICANT: SCHREIBER, STUART L.
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: HUV-037.01
; CURRENT APPLICATION NUMBER: US/09/800,187
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,802
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-187-54
Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 1 DLDA 4

Db 3 DLDA 6

RESULT 5

US-09-461-774-20
; Sequence 20, Application US/09461774
; GENERAL INFORMATION:
; APPLICANT: CHAN, Lily
; APPLICANT: CHUNG, Maxey Ching Ming
; APPLICANT: LIM, Renee Lay Hong
; TITLE OF INVENTION: Bacterial-derived molecules and therapeutic and
; FILE OF INVENTION: diagnostic uses therefor
; FILE REFERENCE: 1781-0180P
; CURRENT APPLICATION NUMBER: US/09/461,774
; CURRENT FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-461-774-20

Query Match 100.0%; Score 20; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 7 DLDA 10

RESULT 6

US-08-227-772-135
; Sequence 135, Application US/08227772
; GENERAL INFORMATION:
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET SUITE 510
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,772
FILING DATE: 14-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/881,396
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: MANDRAGOURAS, AMY E.
REGISTRATION NUMBER: P36,207
REFERENCE/DOCKET NUMBER: IMI-012/IPC-017C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-227-772-135

Query Match 100.0%; Score 20; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 5 DLDA 8

RESULT 7

US-08-445-307A-135
; Sequence 135, Application US/08445307A
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307A
FILING DATE: 07 June 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.60S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-445-307A-135

Query Match 100.0%; Score 20; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 5 DLDA 8

RESULT 8

US-09-273-597-3
; Sequence 3, Application US/09273597
; GENERAL INFORMATION:

```
; APPLICANT: Verdine, Greg L.
; APPLICANT: Chytil, Milan
; APPLICANT: Malinky, Tiffany
; APPLICANT: Didluk, Mary T.
; TITLE OF INVENTION: SYNTHESIS OF COMPOUNDS AND LIBRARIES OF
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 00246-258001
; CURRENT APPLICATION NUMBER: US/09/273,597
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079,035
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-273-597-3

Query Match          100.0%; Score 20; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
   ||||
Db 1 DLDA 4

RESULT 9
PCT-US98-20991-4
; Sequence 4; Application PC/TUS9820991
; GENERAL INFORMATION:
; APPLICANT: New England Medical Center Hospitals, Inc.
; TITLE OF INVENTION: STRUCTURE-BASED RATIONAL DESIGN OF COMPOUNDS TO INHIBIT
; TITLE OF INVENTION: PAPILLOMA VIRUS INFECTION
; FILE REFERENCE: 00398/135W01
; CURRENT APPLICATION NUMBER: PCT/US98/20991
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: US 60/961,295
; EARLIER FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-20991-4

Query Match          100.0%; Score 20; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
   ||||
Db 3 DLDA 6

RESULT 10
US-09-684-883-22
; Sequence 22; Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
```

```
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-684-883-22

Query Match          100.0%; Score 20; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
   ||||
Db 12 DLDA 15

RESULT 11
US-09-684-883-23
; Sequence 23; Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US/08/913.362
 FILING DATE: 13-NOV-1997
 APPLICATION NUMBER: US 08/406.362
 FILING DATE: 17-MAR-1995
 APPLICATION NUMBER: US 60/001.983
 FILING DATE: 04-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 047998/0128
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Neisseria meningitidis
 STRAIN: 608B
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-684-883-23

Query Match 100.0%; Score 20; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 Db 2 DLDA 5

RESULT 12
 US-08-437-413-2
 Sequence 2, Application US/08437413
 GENERAL INFORMATION:
 APPLICANT: PERRYMAN, M. BENJAMIN
 APPLICANT: WU, ALAN
 APPLICANT: FRIEDMAN, DAVID
 APPLICANT: HAMBURG, ROBERT
 APPLICANT: ROBERTS, ROBERT
 TITLE OF INVENTION: METHOD OF DETERMINING SERUM OR
 TITLE OF INVENTION: PLASMA MITOCHONDRIAL CREATINE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD, WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/437,413
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/007,994
 FILING DATE: JANUARY 11, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BARBARA S. KITCHELL
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: BAYM:008/KIT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-320-7200

TELEFAX: 512-474-7577
 TELEX: NOT APPLICABLE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acid residues
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-437-413-2

Query Match 100.0%; Score 20; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 Db 8 DLDA 11

RESULT 13
 PCT-US01-00663-38679
 Sequence 38679, Application PC/TUS0100663
 GENERAL INFORMATION:
 APPLICANT: Molecular Dynamics, Inc.
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
 FILE REFERENCE: PB 0004 WO 7
 CURRENT APPLICATION NUMBER: PCT/US01/00663
 CURRENT FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 04 February 2000 (04..02.00)
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 26 May 2000 (26.05.00)
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 03 August 2000 (03.08.00)
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 03 October 2000 (03.10.00)
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 27 September 2000 (27.09.00)
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 21 September 2000 (21.09.00)
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 30 June 2000 (30.06.00)
 NUMBER OF SEQ ID NOS: 38837
 SOFTWARE: Molecular Dynamics Sequence Listing Engine
 SEQ ID NO 38679
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL133246.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
 OTHER INFORMATION: EST_HUMAN HIT: AUL17241.1, EVALUATE 2.50e-01
 PCT-US01-00663-38679

Query Match 100.0%; Score 20; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 Db 3 DLDA 6

RESULT 14
 US-08-237-363-24
 Sequence 24, Application US/08237363
 GENERAL INFORMATION:
 APPLICANT: DOSCH, HANS MICHAEL

;; TITLE OF INVENTION: METHODS FOR CONTROLLING T LYMPHOCYTE
;; TITLE OF INVENTION: MEDIATED IMMUNE RESPONSES
;; NUMBER OF SEQUENCES: 29
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BAKER & BOTTS
;; STREET: The Warner, 1299 Pennsylvania Avenue, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20004-2400
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/237/363
;; FILING DATE: 03-MAY-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Remenick, James
;; REGISTRATION NUMBER: 36902
;; REFERENCE/DOCKET NUMBER: 19060-0104
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-639-7700
;; TELEFAX: 202-639-7890
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-237-363-24

Query Match 100.0%; Score 20; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||
Db 8 DLDA 11

RESULT 15
US-09-299-473A-2
; Sequence 2, Application US/09299473A
; GENERAL INFORMATION:
; APPLICANT: Twardzik, Daniel R
; APPLICANT: Felker, Thomas S
; APPLICANT: Stefan, Paskell L
; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR
; TITLE OF INVENTION: STIMULATING STEM CELL PROLIFERATION AND MIGRATION
; FILE REFERENCE: STEM1100
; CURRENT APPLICATION NUMBER: US/09/299,473A
; CURRENT FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-299-473A-2

Query Match 100.0%; Score 20; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||
Db 15 DLDA 18

RESULT 16
US-09-864-761-42568
; Sequence 42568, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rann, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42568
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL13246.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-09-864-761-42568

Query Match 100.0%; Score 20; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||

Db 3 DLDA 6

RESULT 17

US-10-182-993-37608
; Sequence 37608, Application US/10182993
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 2
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/182,993
; PRIOR FILING DATE: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37811
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 37608
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-10-182-993-37608

Query Match 100.0%; Score 20; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 3 DLDA 6

RESULT 18

US-10-182-995-29040
; Sequence 29040, Application US/10182995
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 1
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/182,995
; PRIOR FILING DATE: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 29119
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 29040
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-10-182-995-29040

Query Match 100.0%; Score 20; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 3 DLDA 6

RESULT 19

US-10-182-997-26863
; Sequence 26863, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: PB 0004 WO 10
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/182,997
; PRIOR FILING DATE: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26863
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-10-182-997-26863

Query Match 100.0%; Score 20; DB 25; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 20

US-10-203-134-38471
; Sequence 38471, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 38471
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; FILE REFERENCE: PB 0004 WO 3
US-10-203-134-38471

Query Match 100.0%; Score 20; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 21

US-10-203-136-38459
; Sequence 38459, Application US/10203136
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 3
US-10-203-136-38459

; CURRENT APPLICATION NUMBER: US/10/203,136
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 38459
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; FILE REFERENCE: PB 0004 WO 7
US-10-203-136-38459

Query Match 100.0%; Score 20; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 22

US-10-203-137-38679
; Sequence 38679, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: PB 0004 WO 7
US-10-203-137-38679
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 38679
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: MAP TO AL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-10-203-137-38679

Query Match 100.0%; Score 20; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 23
US-10-203-139-37058
; Sequence 37058, Application US/10203139
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
; FILE REFERENCE: PB 0004 WO 4
; CURRENT APPLICATION NUMBER: US/10/203.139
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37156
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 37058
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133246.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AU117241.1, EVALUE 2.50e-01
US-10-203-139-37058

Query Match 100.0%; Score 20; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 24
US-09-512-563-43
; Sequence 43, Application US/09512563
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan

; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-A
; CURRENT APPLICATION NUMBER: US/09/512,563
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived
; OTHER INFORMATION: peptide
US-09-512-563-43

Query Match 100.0%; Score 20; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 7 DLDA 10

RESULT 25
US-09-512-563A-43
; Sequence 43, Application US/09512563A
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-A
; CURRENT APPLICATION NUMBER: US/09/512,563A
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived
; OTHER INFORMATION: peptide
US-09-512-563A-43

Query Match 100.0%; Score 20; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 7 DLDA 10

RESULT 26
US-09-512-563C-43
; Sequence 43, Application US/09512563C
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-A
; CURRENT APPLICATION NUMBER: US/09/512,563C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: GPIII derived
US-09-512-563C-43

Query Match 100.0%; Score 20; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 7 DLDA 10

RESULT 27

US-07-698-925A-1
Sequence 1, Application US/07698925A

GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji,
APPLICANT: Benedict, William F.,
APPLICANT: Hu, Shi-Xue
TITLE OF INVENTION: Retinoblastoma Protein Immunochemical
TITLE OF INVENTION: Stain and Method
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vaden, Eickenroht, Thompson & Boulware
STREET: One Riverway
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77056-1903

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/698,925A
FILING DATE: 19910513
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/338,289, US 07/508,051
FILING DATE: 14-APR-1989, 11-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Boulware, Margaret A.
REGISTRATION NUMBER: 28708
REFERENCE/DOCKET NUMBER: BAYAO08CIP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 961-3525
TELEFAX: (713) 961-3723

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: polypeptide

FEATURE:
NAME/KEY: EXON 10 region - retinoblastoma protein
LOCATION: 322 - 341
OTHER INFORMATION: epitope of retinoblastoma protein
US-07-698-925A-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 9 DLDA 12

RESULT 28

US-08-944-147-22
Sequence 22, Application US/08944147

GENERAL INFORMATION:
APPLICANT: Jackson, David C.
APPLICANT: O'Brien-Simpson, Neil M.
APPLICANT: Brown, Lorena E.
APPLICANT: Ede, Nicholas J.
APPLICANT: Brandy, Evelyn R.
APPLICANT: Good, Michael F.
APPLICANT: Zeng, Weiquang
TITLE OF INVENTION: POLYMERS INCORPORATION PEPTIDES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,147
FILING DATE: 06-OCT-1997
CLASSIFICATION: 526
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: FBRC:006

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7544
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-944-147-22

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|||||
Db 4 DLDA 7

RESULT 29

US-08-944-147-22
Sequence 22, Application US/08944147A

GENERAL INFORMATION:
APPLICANT: JACKSON, DAVID C.
APPLICANT: O'BRIEN-SIMPSON, NEIL M.
APPLICANT: BROWN, LORENA E.
APPLICANT: EDE, NICHOLAS J.
APPLICANT: BRANDT, EVELYN R.
APPLICANT: GOOD, MICHAEL F.
TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
FILE REFERENCE: FBRC:006
CURRENT APPLICATION NUMBER: US/08/944,147A
CURRENT FILING DATE: 1997-10-06
EARLIER APPLICATION NUMBER: P05071
EARLIER FILING DATE: 1997-02-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 20
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-08-944-147-22

Query Match
 Best Local Similarity 100.0%; Score 20; DB 13; Length 20;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 Db 4 DLDA 7

RESULT 30
 US-10-044-034-22
 Sequence 22, Application US/10044034
 GENERAL INFORMATION:
 APPLICANT: JACKSON, DAVID C.
 APPLICANT: O'BRIEN-SIMPSON, NEIL M.
 APPLICANT: BROWN, LORENA E.
 APPLICANT: EDE, NICHOLAS J.
 APPLICANT: BRANDT, EVELYN R.
 APPLICANT: GOOD, MICHAEL F.
 TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
 FILE REFERENCE: FBRC:006
 CURRENT APPLICATION NUMBER: US/10/044,034
 CURRENT FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: P05071
 PRIOR FILING DATE: 1997-02-11
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptides
 US-10-044-034-22

Query Match
 Best Local Similarity 100.0%; Score 20; DB 24; Length 20;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 Db 4 DLDA 7

RESULT 31
 US-07-946-304-2
 Sequence 2, Application US/07946304
 GENERAL INFORMATION:
 APPLICANT: Fung, Y.K.
 TITLE OF INVENTION: Cell-Cycle-Dependent Regulation of
 Phosphorylation of the Human Retinoblastoma Gene Product
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gray Cary Ware & Freidenrich
 STREET: 401 "B" Street, Suite 1700
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92101-4297
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/946,304
 FILING DATE: 11-NOV-1992
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Brotman, Harris F.
 REGISTRATION NUMBER: 35,461
 REFERENCE/DOCKET NUMBER: P00050USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-699-3630
 TELEFAX: 619-236-1048
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 2..21
 OTHER INFORMATION: /note= "Corresponds to amino acids
 322 to 341 in Sequence ID No. 1"
 US-07-946-304-2

Query Match
 Best Local Similarity 100.0%; Score 20; DB 3; Length 21;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 Db 10 DLDA 13

RESULT 32
 US-07-969-314A-10
 Sequence 10, Application US/07969314A
 GENERAL INFORMATION:
 APPLICANT: ROOS, Maria H.
 TITLE OF INVENTION: SPECIFIC DNA SEQUENCE OF A NEMATODE
 TITLE OF INVENTION: WHICH CAN BE USED FOR THE DIAGNOSIS OF INFECTION WITH THE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: VA
 COUNTRY: US
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/969,314A
 FILING DATE: 15-APR-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NL 9001832
 FILING DATE: 16-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/NL91/00153
 FILING DATE: 15-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: B036107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-969-314A-10

Query Match          100.0%; Score 20; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 9 DLDA 12

RESULT 33
US-09-080-428-9
; Sequence 9, Application US/09080428
; GENERAL INFORMATION:
; APPLICANT: Golightly, Elizabeth,
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,428
; FILING DATE: 18-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Starnes, Robert L.
; REGISTRATION NUMBER: 41,324
; REFERENCE/DOCKET NUMBER: 5536,000-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; US-09-080-428-9

Query Match          100.0%; Score 20; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 8 DLDA 11

RESULT 34
US-09-724-059-530377
; Sequence 530377, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yuen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 530377

; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 530377

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
; US-09-724-059-530377

Query Match          100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 14 DLDA 17

RESULT 35
US-09-724-059-530378
; Sequence 530378, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yuen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 530378
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
; US-09-724-059-530378

Query Match          100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 14 DLDA 17

RESULT 36
US-09-724-059-530379
; Sequence 530379, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yuen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 530379
```

; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-530379

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 14 DLDA 17

RESULT 37
US-09-724-059-535338
; Sequence 535338, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 535338
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-535338

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 14 DLDA 17

RESULT 38
US-09-724-059-538495
; Sequence 538495, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 538495
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-538495

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
||||
Db 14 DLDA 17

RESULT 39
US-09-724-059-538496
; Sequence 538496, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 538496
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-538496

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 14 DLDA 17

RESULT 40
US-09-724-059-559241
; Sequence 559241, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 559241
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559241

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 14 DLDA 17

RESULT 41
US-09-724-059-559242

; Sequence 559242, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 559242
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559242

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 42

US-09-724-059-559243
; Sequence 559243, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 559243
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559243

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 43

US-09-724-059-559244
; Sequence 559244, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 559244
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559244

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 44

US-09-724-059-559245
; Sequence 559245, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 559245
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559245

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 14 DLDA 17

RESULT 45

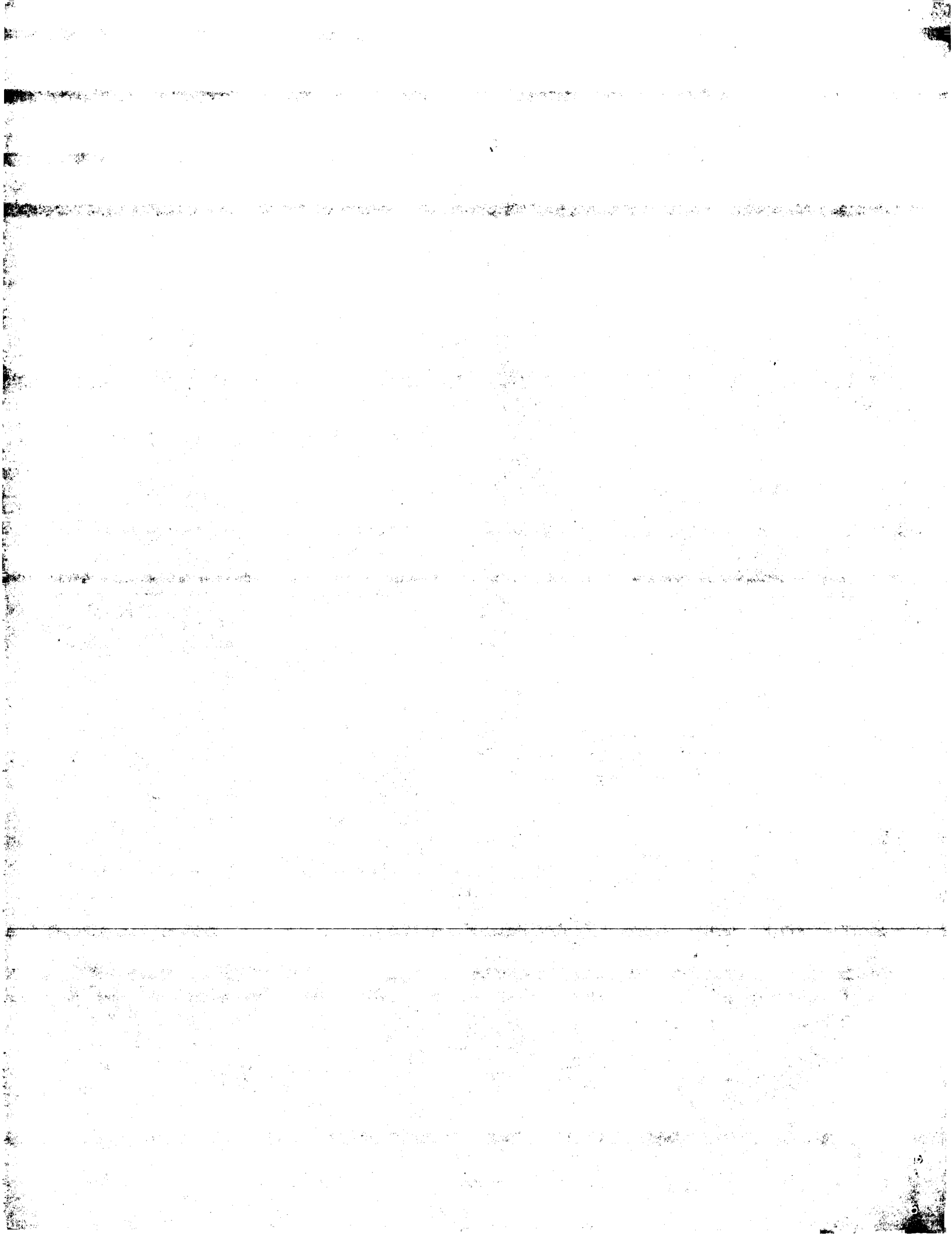
US-09-724-059-559246
; Sequence 559246, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: Macallister
; SEQ ID NO 559246
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-559246

Query Match 100.0%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDA 4
 ||||
Db 14 DLDA 17

Search completed: February 6, 2003, 11:37:32
Job time : 135.167 secs



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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:19:49 ; Search time 14 seconds
(without alignments)
23.165 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dllda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 1507

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	15	6	US-10-169-026-14
2	20	100.0	18	1	PCT-US02-00667A-95
3	20	100.0	19	6	US-10-270-837-43
4	20	100.0	19	6	US-10-270-877-43
5	20	100.0	33	5	US-09-684-758-9
6	20	100.0	33	5	US-09-684-758-11
7	20	100.0	33	5	US-09-684-758-13
8	20	100.0	33	5	US-09-684-758-15
9	20	100.0	50	5	US-09-492-935C-2
10	20	100.0	51	1	PCT-US02-32727-25319
11	20	100.0	51	6	US-10-057-498-25319
12	20	100.0	53	1	PCT-US02-32727-4206
13	20	100.0	53	6	US-10-057-498-4206
14	20	100.0	57	1	PCT-US02-32727-18426
15	20	100.0	57	5	US-09-513-999C-5509
16	20	100.0	57	6	US-10-057-498-18426
17	20	100.0	61	1	PCT-US02-32727-18873
18	20	100.0	61	5	US-09-950-084-5891
19	20	100.0	61	6	US-10-057-498-18873
20	20	100.0	64	1	PCT-US02-32727-488
21	20	100.0	64	6	US-10-057-498-488
22	20	100.0	72	1	PCT-US02-32727-22782
23	20	100.0	72	6	US-10-270-837-48
24	20	100.0	72	6	US-10-270-837-52
25	20	100.0	72	6	US-10-270-837-61
26	20	100.0	72	6	US-10-270-877-48

27	20	100.0	72	6	US-10-270-877-52	Sequence 52, Appl
28	20	100.0	72	6	US-10-270-877-61	Sequence 61, Appl
29	20	100.0	72	6	US-10-057-498-22782	Sequence 22782, A
30	20	100.0	73	1	PCT-US02-32727-22479	Sequence 22479, A
31	20	100.0	73	6	US-10-057-498-22479	Sequence 22479, A
32	20	100.0	74	5	US-09-513-999C-5464	Sequence 5464, Ap
33	20	100.0	74	5	PCT-US02-32727-10139	Sequence 10139, A
34	20	100.0	77	1	US-09-513-999C-6393	Sequence 6393, Ap
35	20	100.0	77	5	US-10-057-498-10139	Sequence 10139, A
36	20	100.0	77	6	PCT-US02-32727-18061	Sequence 18061, A
37	20	100.0	78	1	PCT-US02-32727-23116	Sequence 23116, A
38	20	100.0	78	6	US-10-057-498-18061	Sequence 18061, A
39	20	100.0	78	6	US-10-057-498-23116	Sequence 23116, A
40	20	100.0	79	1	PCT-US02-32727-17661	Sequence 17661, A
41	20	100.0	79	6	US-10-057-498-17661	Sequence 17661, A
42	20	100.0	81	5	US-09-134-000C-4519	Sequence 4519, Ap
43	20	100.0	81	5	US-09-134-000C-4519	Sequence 4519, Ap
44	20	100.0	81	5	US-09-134-000C-4519	Sequence 4519, Ap
45	20	100.0	83	1	PCT-US02-32727-26672	Sequence 26672, A

ALIGNMENTS

RESULT 1

US-10-169-026-14
; Sequence 14, Application US/10169026
; GENERAL INFORMATION:
; APPLICANT: SATO, Atsushi
; TITLE OF INVENTION: Cytokine-Like Peptide
; FILE REFERENCE: 1254-0209P
; CURRENT APPLICATION NUMBER: US/10/169,026
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: JP 369990/1999
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09278
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide SYR6-N14
US-10-169-026-14

Query Match 100.0%; Score 20; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

RESULT 2

PCT-US02-00667A-95
; Sequence 95, Application PC/TUS0200667A
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF MARYLAND, COLLEGE PARK
; TITLE OF INVENTION: METHODS FOR DETERMINING RING NUMBER IN CAROTENOIDS BY
; FILE REFERENCE: 108172-00055
; CURRENT APPLICATION NUMBER: PCT/US02/00667A
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 60/261,473
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 18

; TYPE: PRT
; ORGANISM: Arabidopsis sp.
PCT-US02-00667A-95

Query Match 100.0%; Score 20; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 13 DLDA 16

RESULT 3

US-10-270-837-43
; Sequence 43, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived
US-10-270-837-43

Query Match 100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 7 DLDA 10

RESULT 4

US-10-270-877-43
; Sequence 43, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived
US-10-270-877-43

Query Match 100.0%; Score 20; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 7 DLDA 10

RESULT 5

US-09-684-758-9
; Sequence 9, Application US/09684758
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H.
; APPLICANT: Frick, Inga-Maria
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 100084.413US
; CURRENT APPLICATION NUMBER: US/09/684,758
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-684-758-9

Query Match 100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 28 DLDA 31

RESULT 6

US-09-684-758-11
; Sequence 11, Application US/09684758
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H.
; APPLICANT: Frick, Inga-Maria
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 100084.413US
; CURRENT APPLICATION NUMBER: US/09/684,758
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-684-758-11

Query Match 100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 28 DLDA 31

RESULT 7

US-09-684-758-13
; Sequence 13, Application US/09684758
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H.
; APPLICANT: Frick, Inga-Maria
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 100084.413US
; CURRENT APPLICATION NUMBER: US/09/684,758
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13

; LENGTH: 33
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-684-758-13

Query Match 100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 28 DLDA 31

RESULT 8
US-09-684-758-15
; Sequence 15, Application US/09684758
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H.
; APPLICANT: Frick, Inga-Maria
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 100084.413US
; CURRENT APPLICATION NUMBER: US/09/684,758
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-684-758-15

Query Match 100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 28 DLDA 31

RESULT 9
US-09-492-935C-2
; Sequence 2, Application US/09492935C
; GENERAL INFORMATION:
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.
; APPLICANT: TWARDZIK, Daniel
; APPLICANT: PERNET, Andre
; APPLICANT: FELKER, Thomas S.
; APPLICANT: PASKELL, Stefan
; TITLE OF INVENTION: USES OF TGF-alpha AND RELATED POLYPEPTIDES
; FILE REFERENCE: STEM1110-1
; CURRENT APPLICATION NUMBER: US/09/492,935C
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 09/378,567
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-492-935C-2

Query Match 100.0%; Score 20; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 47 DLDA 50

RESULT 10
PCT-US02-32727-25319
; Sequence 25319, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 25319
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-25319

Query Match 100.0%; Score 20; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 20 DLDA 23

RESULT 11
US-10-057-498-25319
; Sequence 25319, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 25319
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-25319

Query Match 100.0%; Score 20; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 20 DLDA 23

RESULT 12
PCT-US02-32727-4206
; Sequence 4206, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shylan
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 4206
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-4206

Query Match 100.0%; Score 20; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 13 DLDA 16

RESULT 13
US-10-057-498-4206
; Sequence 4206, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 4206
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-4206

Query Match 100.0%; Score 20; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 13 DLDA 16

RESULT 14
PCT-US02-32727-18426
; Sequence 18426, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shylan
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 18426
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-18426

Query Match 100.0%; Score 20; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 12 DLDA 15

RESULT 15
US-09-513-999C-5509
; Sequence 5509, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5509
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 43
; OTHER INFORMATION: Xaa-Lys or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 44
; OTHER INFORMATION: Xaa-Lys or Gln
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 45
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 48
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 50
; OTHER INFORMATION: Xaa-Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 51
; OTHER INFORMATION: Xaa-Gln or Arg
US-09-513-999C-5509

Query Match 100.0%; Score 20; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 18 DLDA 21

RESULT 16

US-10-057-498-18426
; Sequence 18426, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 18426
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-18426

Query Match 100.0%; Score 20; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 12 DLDA 15

RESULT 17

PCT-US02-32727-18873
; Sequence 18873, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 18873
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-18873

Query Match 100.0%; Score 20; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 13 DLDA 16

RESULT 18

US-09-950-084-5891
; Sequence 5891, Application US/09950084
; GENERAL INFORMATION:
; APPLICANT: George H. Shimer, Jr.
; APPLICANT: George H. Miller
; APPLICANT: Roberta S. Hare
; APPLICANT: Karen J. Shaw
; TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
; FILE REFERENCE: 1034/1C963US2
; CURRENT APPLICATION NUMBER: US/09/950,084
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/417,811
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/353,718
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/266,557
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,556
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,555
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,542
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,541
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/037,934
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/036,720
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: US 09/036,338
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 7451
; SEQ ID NO 5891
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-5891

Query Match 100.0%; Score 20; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 17 DLDA 20

RESULT 19

US-10-057-498-18873
; Sequence 18873, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 18873
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-18873

Query Match 100.0%; Score 20; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
Db 13 DLDA 16

```

RESULT 20
PCT-US02-32727-488
; Sequence 488, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 488
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-488

Query Match      100.0%; Score 20; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 47 DLDA 50

RESULT 21
US-10-057-498-488
; Sequence 488, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 488
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-488

Query Match      100.0%; Score 20; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 47 DLDA 50

RESULT 22
PCT-US02-32727-22782
; Sequence 22782, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir

```

; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPDIII-V
US-10-270-837-52

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|||
Db 60 DLDA 63

RESULT 25

US-10-270-837-61
; Sequence 61, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-837-61

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|||
Db 60 DLDA 63

RESULT 26

US-10-270-877-48
; Sequence 48, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: GPDIII
US-10-270-877-48

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|||
Db 60 DLDA 63

RESULT 27

US-10-270-877-52
; Sequence 52, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPDIII-V
US-10-270-877-52

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|||
Db 60 DLDA 63

RESULT 28

US-10-270-877-61
; Sequence 61, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-877-61

Query Match 100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|||
Db 60 DLDA 63

```
RESULT 29
US-10-057-498-22782
; Sequence 22782, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 22782
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-22782

Query Match      100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 62 DLDA 65

RESULT 30
PCT-US02-32727-22479
; Sequence 22479, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 22479
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-22479

Query Match      100.0%; Score 20; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 60 DLDA 63

RESULT 31
US-10-057-498-22479
; Sequence 22479, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
```

```
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 22479
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-22479

Query Match      100.0%; Score 20; DB 6; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 60 DLDA 63

RESULT 32
US-09-513-999C-5464
; Sequence 5464, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5464
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 7
; OTHER INFORMATION: Xaa-Arg or Thr
US-09-513-999C-5464

Query Match      100.0%; Score 20; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 31 DLDA 34

RESULT 33
US-09-513-999C-5490
; Sequence 5490, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5490
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
```

; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 56
; OTHER INFORMATION: Xaa-Lys or Asn
US-09-513-999C-5490

Query Match 100.0%; Score 20; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 60 DLDA 63

RESULT 34
PCT-US02-32727-10139

; Sequence 10139, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siquing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 10139
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-10139

Query Match 100.0%; Score 20; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 70 DLDA 73

RESULT 35
US-09-513-999C-6393
; Sequence 6393, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6393
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: UNSURE
; LOCATION: 66
; OTHER INFORMATION: Xaa-His or Leu or Pro or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa-Gly or Val
US-09-513-999C-6393

Query Match 100.0%; Score 20; DB 5; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 3 DLDA 6

RESULT 36

US-10-057-498-10139
; Sequence 10139, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 10139
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-10139

Query Match 100.0%; Score 20; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
Db 70 DLDA 73

RESULT 37

PCT-US02-32727-18061
; Sequence 18061, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siquing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 18061
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-18061

Query Match 100.0%; Score 20; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
Db 42 DLDA 45

RESULT 38

PCT-US02-32727-23116
; Sequence 23116, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Shigang

; APPLICANT: Jen, Shyian

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 23116

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-23116

Query Match 100.0%; Score 20; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
Db 67 DLDA 70

RESULT 39

US-10-057-498-18061

; Sequence 18061, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 18061

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-18061

Query Match 100.0%; Score 20; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
 ||||
Db 42 DLDA 45

RESULT 40

US-10-057-498-23116

; Sequence 23116, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 23116

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-23116

Query Match 100.0%; Score 20; DB 6; Length 78;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

 ||||

Db 67 DLDA 70

RESULT 41

PCT-US02-32727-17661

; Sequence 17661, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Shigang

; APPLICANT: Jen, Shyian

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 17661

; LENGTH: 79

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-17661

Query Match 100.0%; Score 20; DB 1; Length 79;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

 ||||

Db 37 DLDA 40

RESULT 42

US-10-057-498-17661

; Sequence 17661, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17661
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-17661

Query Match 100.0%; Score 20; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 37 DLDA 40

RESULT 43

US-09-134-000C-4519
; Sequence 4519, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4519
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4519

Query Match 100.0%; Score 20; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 54 DLDA 57

RESULT 44

US-09-134-000C-4519
; Sequence 4519, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4519
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4519

Query Match 100.0%; Score 20; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 54 DLDA 57

RESULT 45

PCT-US02-32727-26672
; Sequence 26672, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Shiqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; FILE OF INVENTION: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 26672
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-26672

Query Match 100.0%; Score 20; DB 1; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 9 DLDA 12

Search completed: February 6, 2003, 11:39:01
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 ; Search time 10.5 seconds
(without alignments)
36.623 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2360

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	26	2	PL0027
2	20	100.0	28	2	S15235
3	20	100.0	57	2	D44530
4	20	100.0	60	2	H41476
5	20	100.0	61	2	A36916
6	20	100.0	66	2	T35138
7	20	100.0	69	2	D86682
8	20	100.0	70	2	C86462
9	20	100.0	71	1	H70799
10	20	100.0	72	2	D86570
11	20	100.0	72	2	A72055
12	20	100.0	74	2	D95048
13	20	100.0	74	2	B97919
14	20	100.0	75	2	T17107
15	20	100.0	76	2	T25085
16	20	100.0	77	2	C95004
17	20	100.0	77	2	F97876
18	20	100.0	79	2	S38756
19	20	100.0	79	2	C87558
20	20	100.0	79	2	B64614
21	20	100.0	79	2	C71901
22	20	100.0	80	2	A90957
23	20	100.0	80	2	H75472
24	20	100.0	80	2	E85805
25	20	100.0	81	2	A49736
26	20	100.0	82	2	F75326
27	20	100.0	84	2	E84345
28	20	100.0	84	2	B97300
29	20	100.0	85	2	A70898

30	20	100.0	86	2	C95304
31	20	100.0	87	2	F40361
32	20	100.0	87	2	T43570
33	20	100.0	87	2	H70079
34	20	100.0	87	2	AF3030
35	20	100.0	91	2	E90766
36	20	100.0	91	2	F85716
37	20	100.0	92	2	E83305
38	20	100.0	92	2	JC4564
39	20	100.0	93	2	E83630
40	20	100.0	94	2	AC3252
41	20	100.0	95	2	S24146
42	20	100.0	96	2	S71519
43	20	100.0	96	2	H83065
44	20	100.0	97	2	H98254
45	20	100.0	98	2	S61079

ALIGNMENTS

RESULT 1

PL0027

M protein pepM19 - Streptococcus sp. (fragment)

C:Species: Streptococcus sp.

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997

C:Accession: PL0027

R:Bronze, M.S.; Beachey, E.H.; Dale, J.B.

J. Exp. Med. 167, 1849-1859, 1988

A:Title: Protective and heart-crossreactive epitopes located within the NH2 terminus of the M protein of Streptococcus pneumoniae

A:Reference number: PL0027; MUID:88258373; PMID:2455015

A:Accession: PL0027

A:Molecule type: protein

A:Residues: 1-26 <BRO>

C:Superfamily: M5 protein

C:Keywords: virulence factor

Query Match 100.0%; Score 20; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 18 DLDA 21

RESULT 2

S15235

hypothetical protein - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: S15235

R:Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.

Mol. Microbiol. 5, 163-171, 1991

A:Title: Molecular characterization of the gor gene encoding glutathione reductase

A:Reference number: S15235; MUID:91194546; PMID:1849605

A:Accession: S15235

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-28 <PER>

A:Cross-references: EMBL:X54201; NID:g45324; PIDN:CAA38121.1; PID:g45325

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 28;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 14 DLDA 17

RESULT 3

D44530
T-cell receptor alpha chain V region (BTA40) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: D44530
R:Ishiguro, N.; Tanaka, A.; Shinagawa, M.
Immunogenetics 31, 57-60, 1990
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.
A:Reference number: A45893; MUID:90129157; PMID:2137108
A:Accession: D44530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-57 <ISH>
A:Cross-references: GB:D90022; NID:g217632; PIDN:BAAL4072.1; PID:g217633
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 100.0%; Score 20; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 1 DLDA 4

RESULT 4
H41476
probable antigen 8 - Mycobacterium leprae (fragment)
C:Species: Mycobacterium leprae
C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993
C:Accession: H41476
R:Hartkeerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.
Infect. Immun. 58, 2821-2827, 1990
A:Title: Selection and characterization of recombinant clones that produce Mycobacterium
A:Reference number: A41476; MUID:90354041; PMID:1696931
A:Accession: H41476
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-60 <HAR>

Query Match 100.0%; Score 20; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 45 DLDA 48

RESULT 5
A36916
orf61 5' of int - Streptomyces lividans.
C:Species: Streptomyces lividans
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: A36916
R:Brasch, M.A.; Pettis, G.S.; Lee, S.C.; Cohen, S.N.
J. Bacteriol. 175, 3067-3074, 1993
A:Title: Localization and nucleotide sequences of genes mediating site-specific recombination
A:Reference number: A36916; MUID:93259953; PMID:8387993
A:Accession: A36916
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <BRA>
A>Note: sequence extracted from NCBI backbone (NCBIN:131954, NCBI:P:131955)

Query Match 100.0%; Score 20; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 49 DLDA 52

RESULT 6 T35138

hypothetical protein SC4H8.07c SC4H8.07c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35138
R:Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z21569

A:Accession: T35138
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-66 <HAR>
A:Cross-references: EMBL:AL020958; PIDN:CAAL15874.1; GSPDB:GN00070; SCOEDB:SC4H8.07c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC4H8.07c

Query Match 100.0%; Score 20; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 7 DLDA 10

RESULT 7 D86682

prophage pil protein 25 [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: D86682
R:Botolin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Welissenbach, J.;
Genome Res. 11, 751-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lact
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86682
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <STO>
A:Cross-references: GB:AE005176; PID:g12723339; PIDN:AAK04558.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pil25

Query Match 100.0%; Score 20; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 41 DLDA 44

RESULT 8 C86462

unknown protein, 62609-62906 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86462
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C86462
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-70 <STO>
 A:Cross-references: GB:AE005172; NID:g6957515; PIDN:AAF32437.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 DB 25 DLDA 28

RESULT 9

H70799
 Integrase-related protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: H70799
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Spares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: H70799
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-71 <COL>
 A:Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18073.1; PID:g296017
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3751
 C:Superfamily: Mycobacterium tuberculosis integrase-related protein

Query Match 100.0%; Score 20; DB 1; Length 71;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 DB 55 DLDA 58

RESULT 10

D86570
 L23 ribosomal protein [imported] - Chlamydomophila pneumoniae (strain J138)
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: D86570
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishioka, Y. Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: D86570
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-72 <STO>
 A:Cross-references: GB:BA000008; NID:g9879011; PIDN:BAA98846.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: r129

Query Match 100.0%; Score 20; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 DB 18 DLDA 21

RESULT 11

A72055
 ribosomal protein L29 CP0108 [imported] - Chlamydomophila pneumoniae (strains CWL029
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: A72055; H81611
 R:Kalan, S.; Michell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: A72055
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-72 <ARN>
 A:Cross-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAI8778.1; PID:g
 A:Experimental source: strain CWL029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H
 , C.; Dodson, R.; Giehn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sal
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: H81611
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-72 <REA>
 A:Cross-references: GB:AE002173; GB:AE002161; NID:g7189033; PIDN:AAF37991.1; PID:g
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: r129; CP0108

Query Match 100.0%; Score 20; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 DB 18 DLDA 21

RESULT 12

D95048
 acyl carrier protein [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C:Accession: D95048
 R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtz
 nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: D95048
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-74 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK74581.1; PID:g14971887; GSPDB:GN00164; T
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0418

Query Match 100.0%; Score 20; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 ||||
 DB 30 DLDA 33

```
RESULT 13
B97919
acyl carrier protein [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: B97919
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; F
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99182.1; PID:g15457939; GSPDB:GN00174
C:Genetics:
A:Gene: acp

Query Match 100.0%; Score 20; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 30 DLDA 33

RESULT 14
T17107
proline rich protein - apple tree (fragment)
C:Species: Malus domestica (apple tree)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C:Accession: T17107
R:Dong, Y.H.; Janssen, B.J.; Bielecki, L.L.; Atkinson, R.G.; Morris, B.A.; Gardner, R.C.
J. Am. Soc. Hort. Sci. 122, 752-757, 1997
A:Title: Isolating and characterizing genes differentially expressed early in apple fruit
A:Reference number: Z18681
A:Accession: T17107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-75 <DON>
A:Cross-references: EMBL:U80271; NID:g1732364; PID:g1732365
A:Experimental source: strain Granny Smith
C:Genetics:
A:Gene: PRP
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 100.0%; Score 20; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 31 DLDA 34

RESULT 15
T29085
hypothetical protein SCIC2.36 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T29085
R:Redenbach, M.; Krieser, H.M.; Denapajite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
Mol. Microbiol. 21, 77-96, 1996
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb s
A:Reference number: Z20556; MUID:97000351; PMID:8843436
A:Accession: T29085
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-76 <RED>
A:Cross-references: EMBL:AL031124; NID:el1312893; PID:el1312929; PIDN:CAA20003.1
C:Genetics:
A:Note: SCIC2.36

Query Match 100.0%; Score 20; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 65 DLDA 68

RESULT 16
C95004
acyl carrier protein, probable [imported] - Streptococcus pneumoniae (strain TIGR4
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: C95004
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtz
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95004
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74228.1; PID:g14971502; GSPDB:GN00164; TIG
C:Genetics:
A:Gene: SP0038

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 33 DLDA 36

RESULT 17
F97876
acyl carrier protein [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: F97876
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas,
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F97876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK98842.1; PID:g15457569; GSPDB:GN00174
C:Genetics:
A:Gene: acp

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
```

Db 33 DLDA 36

RESULT 18

S38756

Cytochrome c551 - Ectothiorhodospira halochloris
C:Species: Ectothiorhodospira halochloris
C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 04-Mar-2000
A:Accession: S38756
R:Ambler, R.P.; Meyer, T.E.; Kamen, M.D.
Arch. Biochem. Biophys. 306, 83-93, 1993
A:Title: Amino acid sequences of cytochromes c-551 from the halophilic purple phototroph
A:Reference number: S38755; MUID:94028993; PMID:8215425

A:Accession: S38756

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-79 <AMB>

C:Superfamily: cytochrome c6; cytochrome c6 homolog

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein

F:3-74/Domain: cytochrome c6 homolog <CYC>

F:14.17/Binding site: heme (Cys) (covalent) #status predicted

F:18.55/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 79;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 38 DLDA 41

RESULT 19

C87558

conserved hypothetical protein CC2492 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002

A:Accession: C87558

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: C87558

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-79 <STO>

A:Cross-references: GB:AE005673; NID:g13424047; PIDN:AAK24463.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2492

C:Superfamily: conserved hypothetical protein MJ1593

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 79;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 45 DLDA 48

RESULT 20

B64614

hypothetical protein HP0754 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

A:Accession: B64614

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64614
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <TOM>
A:Cross-references: GB:AE000588; GB:AE000511; NID:g2313880; PIDN:AAD07810.1; PID:g

Query Match 100.0%; Score 20; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 39 DLDA 42

RESULT 21

C71901

hypothetical protein jhp0691 - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

A:Accession: C71901

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith,

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastr

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: C71901

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-79 <ARN>

A:Cross-references: GB:AE001500; GB:AE001439; NID:g4155238; PIDN:AAD06266.1; PID:g

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp0691

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 79;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 39 DLDA 42

RESULT 22

A90957

hypothetical protein ECS2625 [imported] - Escherichia coli (strain O157:H7, substr

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

A:Accession: A90957

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han

gasawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

gsa Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 an

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A90957

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA836048.1; PID:g13362093; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS2625

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 80;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 51 DLDA 54

RESULT 23

H75472

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: H75472

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: H75472

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <WHI>

A:Cross-references: GB:AE001935; GB:AE000513; NID:g6458517; PIDN:AAF10390.1; PID:g645852

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0803

A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 41 DLDA 44

RESULT 24

E85805

unknown protein encoded by prophage CP-933T [imported] - Escherichia coli (strain O157:H

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: E85805

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85805

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <STO>

A:Cross-references: GB:AE005174; NID:gl2515982; PIDN:AAG56905.1; GSPDB:GN00145; UWGP:Z29

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z2973

Query Match 100.0%; Score 20; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 51 DLDA 54

RESULT 25

A49736

collagen alpha 3(IV) chain, short splice form - human (fragment)

N:Contains: collagen alpha 3 (IV) chain, splice form GP-III

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999

C:Accession: A49736; C49736; B45971; S69112

R:Feng, L.; Xia, Y.; Wilson, C.B.

J. Biol. Chem. 269, 2342-2348, 1994

A:Title: Alternative splicing of the NC1 domain of the human alpha3(IV) collagen gene. D

A:Reference number: A49736; MUID:94124597; PMID:8294492

A:Accession: A49736

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 71-81 <FEN1>

A:Accession: C49736

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 22-81 <FEN2>

A:Cross-references: GB:U02520; NID:g408895; PIDN:AAA18943.1; PID:g408896

A:Note: this is the conceptual translation of the nucleic acid submitted to GenBank

R:Bernal, D.; Quinones, S.; Saus, J.

J. Biol. Chem. 268, 12090-12094, 1993

A:Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.

A:Reference number: A45971; MUID:93280184; PMID:8505332

A:Accession: B45971

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 71-81 <BER>

A:Cross-references: PIDN:AA827014.1; PID:g385563

A:Note: sequence extracted from NCBI backbone (NCBIP:133955); sequence incorrectly

R:Penades, J.R.; Bernal, D.; Revert, F.; Johansson, C.; Fresquet, V.J.; Cervera, J. Eur. J. Biochem. 229, 754-760, 1995

A:Title: Characterization and expression of multiple alternatively spliced transcri

ptantigen and one of its alternative forms.

A:Reference number: S69111; MUID:95278230; PMID:7758473

A:Accession: S69112

A:Molecule type: mRNA

A:Residues: 1-45,71-81 <PEN>

C:Comment: For the complete sequence of the long splice form, see PIR:CGH03B.

C:Genetics:

A:Gene: GDB:COL4A3

A:Cross-references: GDB:128351; OMIM:120070

A:Map position: 2q36-2q37

C:Superfamily: collagen alpha 1(IV) chain

C:Keywords: alternative splicing; basement membrane; cell binding; coiled coil; ext

F:1-81/Product: collagen alpha 3(IV) chain, short splice form (fragment) #status p

F:1-45,71-81/Product: collagen alpha 3 (IV) chain, splice form GP-III (fragment) #

F:22-81/Domain: carboxyl-terminal nonhelical, NCI <NC1>

Query Match 100.0%; Score 20; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 69 DLDA 72

RESULT 26

F75326

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: F75326

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, J. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-82 <WHI>

A:Cross-references: GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF11556.1; PID:g

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2009

A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 75 DLDA 78

RESULT 27

E84345

hypothetical protein Vng1944c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: E84345

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithausen, B.; Kellier, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: E84345

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-84 <STO>

A:Cross-references: GB:AE004437; NID:g10581384; PIDN:AAG20129.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1944C

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 84;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 47 DLDA 50

RESULT 28

B97300

hypothetical protein CAC3255 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: B97300

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97300

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-84 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81189.1; PID:g15026329; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3255

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 84;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 67 DLDA 70

RESULT 29

A70898

probable xseB protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: A70898

R:Coie, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrc
Rajandream, M.A.; Rogers, J.; Rutter, K.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete c

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70898

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <COL>

A:Cross-references: GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA1723.1; PID:c

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: xseB

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 85;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 44 DLDA 47

RESULT 30

C95304

hypothetical transposase, partial match [imported] - Sinorhizobium meliloti (stral

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: C95304

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium m

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: C95304

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK64997.1; PID:g14523425; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-H

pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Le

heubault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Y

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMA0643

A:Genome: plasmid

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 86;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 31 DLDA 34

RESULT 31

F40361

virC-region hypothetical protein yscF - Yersinia enterocolitica plasmid pyv

C:Species: Yersinia enterocolitica

C>Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 08-Oct-1999

C:Accession: F40361

R:Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvroit, C.; China, B.; Gustin, A.,

J. Bacteriol. 173, 4994-5009, 1991

A:Title: Analysis of virC, an operon involved in the secretion of Yop proteins by

A:Reference number: A40361; MUID:91317716; PMID:1860816

A:Accession: F40361
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <MUC>
A:Cross-references: GB:M74011; NID:g155549; PIDN:AAC37023.1; PID:g155555
C:Genetics:
A:Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 15 DLDA 18

RESULT 32

T43570

type III secretion protein yscF - Yersinia pestis plasmid pCD1
N:Alternate names: translocation protein F homolog
C:Species: Yersinia pestis
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43570; T42865
R:Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998
A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A:Reference number: 222578; MUID:98422474; PMID:9748454

A:Accession: T43570

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-87 <HUP>

A:Cross-references: EMBL:AF053946; NID:g2996222; PIDN:AAC62549.1; PID:g2996226

A:Experimental source: strain KIM

R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.

Infect. Immun. 66, 4611-4623, 1998

A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia F

A:Reference number: 222273; MUID:98427122; PMID:9746557

A:Accession: T42865

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-87 <PER>

A:Cross-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69778.1; PID:g3822058

A:Experimental source: strain KIM5

C:Genetics:

A:Gene: yscF

A:Genome: plasmid pCD1

Query Match 100.0%; Score 20; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 15 DLDA 18

RESULT 33

H70079

hypothetical protein yxjJ - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000

C:Accession: H70079

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Berte

C:Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, N.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.;
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshi
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subti
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: H70079
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <KUN>
A:Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15919.1; PID:g26;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yxjJ

Query Match 100.0%; Score 20; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 74 DLDA 77

RESULT 34

AF3030

hypothetical protein Atu3950 [imported] - Agrobacterium tumefaciens (strain C58, D
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AF3030

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.;

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; M

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AF3030

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-87 <KUR>

A:Cross-references: GB:AE008689; PIDN:AAL44660.1; PID:g17742285; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu3850

A:Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 35 DLDA 38

RESULT 35

E90766

hypothetical protein ECs1101 [imported] - Escherichia coli (strain O157:H7, subst

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: E90766

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Har

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 ar

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E90766

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034524.1; PID:g13360561; GSPDB:GN00154

A:Residues: 1-91 <HAY>

A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1101

Query Match 100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4
||||
Db 37 DLDA 40

RESULT 36

F85716 unknown protein encoded within prophage CP-9330 [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85716
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85716

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-91 <STO>

A:Cross-references: GB:AE005174; NID:gl21515079; PIDN:AAG56194.1; GSPDB:GN00145; UWGP:Z21

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z2124

Query Match 100.0%; Score 20; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4
||||
Db 37 DLDA 40

RESULT 37

E83305

hypothetical protein PA2723 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: E83305

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bro
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83305

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-92 <STO>

A:Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06111.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2723

Query Match 100.0%; Score 20; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4
||||
Db 64 DLDA 67

RESULT 38

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

JC4564 antifungal protein precursor - Penicillium chrysogenum

C:Species: Penicillium chrysogenum

C:Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000

C:Accession: JC4564

R:Marx, F.; Haas, H.; Reindl, M.; Stoeffler, G.; Lottspeich, F.; Redl, B.

Gene 167, 167-171, 1995

A:Title: Cloning, structural organization and regulation of expression of the Peni

A:Reference number: JC4564; MUID:96144269; PMID:8566771

A:Accession: JC4564

A:Molecule type: mRNA

A:Residues: 1-92 <MAR>

A:Cross-references: GB:U22944; NID:g862384; PIDN:AAA92718.1; PID:g862385

C:Comment: This protein is an abundantly secreted, highly basic, and cysteine-rich

C:Genetics:

A:Gene: paf

A:Introns: 42/3; 72/3

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-37/Domain: propeptide #status predicted <PRS>

F:38-92/Product: antifungal protein #status predicted <MAT>

Query Match 100.0%; Score 20; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4
||||
Db 27 DLDA 30

RESULT 39

E83630

hypothetical protein PA0124 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: E83630

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83630

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-93 <STO>

A:Cross-references: GB:AE004450; GB:AE004091; NID:g9945943; PIDN:AAG03514.1; GSPDB

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0124

Query Match 100.0%; Score 20; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4
||||
Db 12 DLDA 15

RESULT 40

AC3252

agrocipine phosphodiesterase [imported] - Agrobacterium tumefaciens (strain C58,

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AC3252

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; M

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; M

.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-K

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193
A;Accession: AC3252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <KUR>
A;Cross-references: GB:AF008690; PIDN:AA146433.1; PID:g17744230; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: accF
A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 16 DLDA 19

RESULT 41

S24146
S-100 protein P - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S24146; PS0340
R;Becker, T.; Gerke, V.; Kube, E.; Weber, K.
Eur. J. Biochem. 207, 541-547, 1992
A;Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recombinant expression, and characterization of the S-100 protein family
A;Reference number: S24146; MUID:92339442; PMID:1633809
A;Accession: S24146
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-95 <BEC>
A;Cross-references: EMBL:X65614; NID:g36177; PIDN:CAA46566.1; PID:g36178
R;Emoto, Y.; Kobayashi, R.; Akatsuka, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1246-1253, 1992
A;Title: Purification and characterization of a new member of the S-100 protein family from human placenta
A;Reference number: PS0340; MUID:92171935; PMID:1540168
A;Accession: PS0340
A;Molecule type: protein
A;Residues: 1-31, 'T', 33-84, 'X', 86-91 <EMO>
A;Experimental source: placenta
C;Genetics:
A;Gene: GDB:S100P
A;Cross-references: GDB:I34405; OMIM:600614
A;Map position: 4p16-4p16
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; placenta
F:6-40/Domain: calmodulin repeat homology <EF1>
F:49-81/Domain: calmodulin repeat homology <EF2>

Query Match 100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 60 DLDA 63

RESULT 42

S71519
M protein type 19 - Streptococcus pyogenes (fragment)
C;Species: Streptococcus pyogenes
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S71519; S71515
R;Podbielski, A.; Melzer, B.; Lutticken, R.
submitted to the EMBL Data Library, November 1990
A;Description: Application of the polymerase chain reaction to study the M protein(-like) of Streptococcus pyogenes
A;Reference number: S71518
A;Accession: S71519
A;Molecule type: DNA

A;Residues: 1-96 <POD>
A;Cross-references: EMBL:X56609
A;Experimental source: strain J17D/70
R;Podbielski, A.; Melzer, B.; Lutticken, R.
Med. Microbiol. Immunol. 180, 213-227, 1991
A;Title: Application of the polymerase chain reaction to study the M protein(-like) of Streptococcus pyogenes
A;Reference number: S71514; MUID:92149493; PMID:1784271
A;Accession: S71515
A;Molecule type: DNA
A;Residues: 1-42 <POW>
A;Cross-references: EMBL:X56609
A;Experimental source: J17D/70
C;Genetics:
A;Gene: emm19
C;Superfamily: M5 protein

Query Match 100.0%; Score 20; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 61 DLDA 64

RESULT 43

H83065
hypothetical protein PA4642 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83065
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83065
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <STO>
A;Cross-references: GB:AE004878; GB:AE004091; NID:g9950888; PIDN:AA08029.1; GSPDB:PA01
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4642

Query Match 100.0%; Score 20; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 62 DLDA 65

RESULT 44

H98254
hypothetical protein AGR_L1980 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98254
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Gohl, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markel, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; PMID:11743194
A;Accession: H98254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89562.1; PID:g15159447; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L1980

A;Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 45 DLDA 48

RESULT 45

S61079
M protein precursor - Streptococcus pyogenes (serotype M19) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M19
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C;Accession: S61079; S60799
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm1 gene sequences and t
A;Reference number: S61072
A;Accession: S61079
A;Molecule type: DNA
A;Residues: 1-98 <WHA>
A;Cross-references: EMBL:U11959
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60799
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 18-77 <WHW>
A;Cross-references: EMBL:U11959
C;Genetics:
A;Gene: emm19
C;Superfamily: M5 protein
F;1-30/Domain: signal sequence (fragment) #status predicted <SIG>
F;31-98/Product: M protein (fragment) #status predicted <MAP>

Query Match 100.0%; Score 20; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
|
|
|
|
Db 49 DLDA 52

Search completed: February 6, 2003, 11:23:04
Job time : 12.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 5.33333 Seconds
(without alignments)
31.107 Million cell updates/sec

Title: PAT943-2
Perfect score: 20
Sequence: 1 dlda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 948

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	20	100.0	72	1	RL29_CHLPN	Q927f5	chlamydia p
2	20	100.0	74	1	ACP_STRPN	Q9fbc6	streptococc
3	20	100.0	74	1	ACP_STRPY	Q99yd3	streptococc
4	20	100.0	79	1	C551_ECTHL	P38587	ectothiorho
5	20	100.0	85	1	EX7S_MYCTU	O53455	mycobacteri
6	20	100.0	87	1	YSCF_YEREN	Q01247	yersinia en
7	20	100.0	91	1	S112_BOVIN	P79105	bos taurus
8	20	100.0	93	1	AAT_METEX	P52069	methylobact
9	20	100.0	95	1	S10P_HUMAN	P25815	homo sapien
10	20	100.0	98	1	S10Z_HUMAN	Q8wxg8	homo sapien
11	20	100.0	107	1	SSI_STRGI	P28592	streptomyce
12	20	100.0	110	1	GLPE_PSEAE	Q915u8	pseudomonas
13	20	100.0	112	1	AL17_ASFPU	O42799	aspergillus
14	20	100.0	113	1	GLNB_CYACA	Q9tm37	cyanidium c
15	20	100.0	116	1	CH15_DROVI	P13424	drosophila
16	20	100.0	120	1	VATF_HALN1	Q9hne2	halobacteri
17	20	100.0	122	1	YEBF_ECOLI	P33219	escherichia
18	20	100.0	123	1	RNPA_STRBI	P25817	streptomyce
19	20	100.0	123	1	RNPA_STRCO	P48206	streptomyce
20	20	100.0	124	1	VG19_BPMD2	O64212	mycobacteri
21	20	100.0	129	1	CCDP_MAIZE	Q01595	zea mays (m
22	20	100.0	131	1	Y4TP_RHISN	P55499	rhizobium s
23	20	100.0	136	1	RNK_EGOLI	P40679	escherichia
24	20	100.0	137	1	INL2_DROME	Q9vt51	drosophila
25	20	100.0	140	1	ATPE_VIBCH	Q9knh6	vibrio chol
26	20	100.0	140	1	Y4JK_RHISN	P23205	pseudomonas
27	20	100.0	140	1	YK24_PSEAE	Q9k4f6	streptomyce
28	20	100.0	141	1	DTD_STRCO	P06636	xenopus lae
29	20	100.0	141	1	HBA3_XENLA	P08422	xenopus tro
30	20	100.0	141	1	HBA3_XENTR	O53785	mycobacteri
31	20	100.0	142	1	MM55_MYCTU	O87085	streptomyce
32	20	100.0	144	1	RL11_STRAT	P36258	streptomyce
33	20	100.0	144	1	RL11_STRGR		

34	20	100.0	144	1	RL11_STRSQ	Q07975	streptomyce
35	20	100.0	146	1	RBFA_RHILO	Q98b17	rhizobium l
36	20	100.0	152	1	GLBP_CHITH	P11582	chironomus
37	20	100.0	152	1	RS15_ATH	Q08112	arabidopsis
38	20	100.0	152	1	RS15_PODAN	P34737	podospira a
39	20	100.0	154	1	Y194_AQUAE	O86575	aquifex ao
40	20	100.0	155	1	DUT_CAUCR	Q9a253	caulobacter
41	20	100.0	156	1	YS51_MYCTU	O05808	mycobacteri
42	20	100.0	157	1	YE19_MYCTU	P71688	mycobacteri
43	20	100.0	158	1	ATPX_SYNTP6	P08446	synecococc
44	20	100.0	163	1	ATPX_ANASP	P2410	anaeobac sp
45	20	100.0	168	1	FUSE_BURCE	P24130	burkholderi

ALIGNMENTS

RESULT 1
RL29_CHLPN STANDARD; PRT; 72 AA.
ID RL29_CHLPN Q9JQGS;
AC Q927R5: Q9JQGS;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L29.
GN RPMC OR RL29 OR CPN0639 OR CP0108.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL: AE001647; RAD18778.1; -;
DR EMBL: AE002173; RAF37991.1; -;
DR EMBL: AP002547; BAA98846.1; -;
DR TIGR: CP0108; -;
DR InterPro: IPR001854; Ribosomal_L29.

DR PROSITE; PS00579; RIBOSOMAL_L29; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 72 AA; 8197 MW; 1C7E974B83C852C2 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 18 DLDA 21

RESULT 2
ACP_STRPN STANDARD; PRT; 74 AA.
AC Q9FBC6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl carrier protein (ACP).
GN ACP OR SP0418.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R6;
RX MEDLINE=20365714; PubMed=10910344;
RA Heath R.J., Rock C.O.;
RT "A triclosan-resistant bacterial enzyme."
PL Nature 406:145-146(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Tettelin H., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Peterson S., Nelson M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."
RL Science 293:498-506(2001).
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.

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CC EMBL; AF197933; AAF98272.1; -;
CC EMBL; AE007353; AAK74581.1; -;
CC HSSP; P02901; 1ACP.
CC TIGR; SP0418; -;
CC InterPro; IPR003231; Acyl_carrier.
CC InterPro; IPR003880; Ppantne_attach.
CC Pfam; PF00550; pp-binding; 1.

DR ProDom; PD000887; Acyl_carrier; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; FALSE_NEG.
KW Lipid synthesis; Fatty acid biosynthesis; Phosphopantetheine;
KW Complete proteome.
FT BINDING 35 35 PHOSPHOPANTHETHEINE (BY SIMILARITY).
SQ SEQUENCE 74 AA; 8268 MW; E2E9A78567090C14 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 30 DLDA 33

RESULT 3
ACP_STRPY STANDARD; PRT; 74 AA.
AC Q99YD3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl carrier protein (ACP).
GN ACP OR SPY1753 OR SPYM18_1825.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.

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CC EMBL; AE006603; AAK34496.1; -;
CC EMBL; AE010089; AAL98344.1; -;
CC DR
CC DR


```

DR HSSP; P02901; IACP.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Peptide_attach.
DR Pfam; PF00550; pp-binding; 1.
DR PROSITE; PS00087; Acyl_DOMAIN; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; FALSE_NEG.
DR Lipid synthesis; Fatty acid biosynthesis; Phosphopantetheine;
KW Complete proteome.
FT BINDING 35 35 PHOSPHOPANTHETHEINE (BY SIMILARITY).
SQ SEQUENCE 74 AA; 8343 MW; 41D7F7F23065B44 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 4
C551_ECTHL
ID C551_ECTHL STANDARD; PRT; 79 AA.
AC P38587;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c-551 (C551).
OS Ectothiorhodospira halochloris.
OC Bacteria; Proteobacteria; gamma subdivision; Ectothiorhodospiraceae;
OC Halorhodospira.
OX NCBI_TaxID=1052;
RN [1]
RP SEQUENCE.
RX MEDLINE=94028993; PubMed=8215425;
RA Ambler R.P., Meyer T.E., Kamen M.D.;
RT "Amino acid sequences of cytochromes c-551 from the halophilic purple
RT phototrophic bacteria, Ectothiorhodospira halophila and E.
RT halochloris."
RL Arch. Biochem. Biophys. 306:83-93(1993).
CC -1- MISCELLANEOUS: ECTOTHIORHODOSPIRA IS A GENUS OF PURPLE, SULFUR,
CC PHOTOSYNTHETIC BACTERIA THAT DEPOSIT SULFUR GLOBULES OUTSIDE THEIR
CC CELLS.
DR PIR; S38756; S38756.
DR HSSP; P00122; 1GKS.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; CytC_C1.
DR Pfam; PF00034; cytochrome_c; 1.
DR PRINTS; PR00607; CYTCHROME_CIE.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme.
FT BINDING 14 14 HEME (COVALENT).
FT BINDING 17 17 HEME (COVALENT).
FT METAL 18 18 IRON (HEME AXIAL LIGAND).
FT METAL 55 55 IRON (HEME AXIAL LIGAND).
SQ SEQUENCE 79 AA; 8355 MW; EA6CEA2EF2BA5995 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 38 DLDA 41

RESULT 5
EX7S_MYCTU
ID EX7S_MYCTU STANDARD; PRT; 85 AA.
AC O53455;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
DE (Exonuclease VII small subunit)...
GN XSEB OR RV1107C OR MT1138 OR MTV017.60C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.B., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
CC ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
CC INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Exonuclease activity cleavage in either 5' to 3'
CC or 3' to 5' direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL021897; CAAL7223.1; -.
DR EMBL; AF006993; AAK45395.1; ALT_INIT.
DR TIGR; MT1138; -.
DR TuberculList; RV1107C; -.
DR InterPro; IPR003761; Exonuc_VII_S.
DR Pfam; PF02609; Exonuc_VII_S; 1.
DR TIGRFAMs; TIGR01280; xseB; 1.
DR TIGRFAMs; TIGR01280; xseB; 1.
KW Hydrolyase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 85 AA; 9322 MW; ACD4756808DA79A8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 44 DLDA 47

RESULT 6

```

YSCF_YEREN
ID YSCF_YEREN STANDARD; PRT; 87 AA.
AC Q01247;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE YOP proteins translocation protein F.
GN YSCF.
OS Yersinia enterocolitica.
OG Plasmid pIV.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-439-80 / Serotype O:9;
RA MEDLINE=91317716; PubMed=1860816;
RX Michiels T., Vancotteghem J.-C., de Rouvroit C., China B., Gustin A.,
RA Boudry P., Cornelis G.R.;
RT "Analysis of virC, an operon involved in the secretion of Yop
proteins by Yersinia enterocolitica.";
RL J. Bacteriol. 173:4994-5009(1991).
CC -1- INDUCTION: AT 37 DEGREES CELSIUS IN THE ABSENCE OF CALCIUM.
CC -1- MISCELLANEOUS: BELONGS TO AN OPERON INVOLVED IN THE TRANSLOCATION
OF YOP PROTEINS ACROSS THE BACTERIAL MEMBRANES OR IN THE SPECIFIC
CONTROL OF THIS FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE MXTH/PRGI/YSCF FAMILY.
CC
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CC
CC EMBL; M74011; AAC37023.1; -
DR PIR; F40361.
KW Virulence; Plasmid; Transport; Protein transport.
SQ SEQUENCE 87 AA; 9449 MW; 90E78542BB267CF6 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 15 DLDA 18

RESULT 7
S112_BOVIN
ID S112_BOVIN STANDARD; PRT; 91 AA.
AC P79105;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
DE (CAAF1) (RAGE binding protein).
GN S100A12 OR CAAF1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oesophagus;
RX MEDLINE=96298783; PubMed=8718672;
RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
RA Nagasaki K.;
RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its
molecular cloning and tissue distribution.";

J. Cell Sci. 109:805-815(1996).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99325504; PubMed=10399917;
RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattery T.,
RA Beach D., McClary J., Nagashima M., Morser J., Stern D.,
RA Schmidt A.M.;
RT "RAGE mediates a novel proinflammatory axis: a central cell surface
receptor for S100/calgranulin polypeptides.";
RL Cell 97:889-901(1999).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC
CC EMBL; D49548; BAA08496.1; -
DR EMBL; AF011757; AAB65423.1; -
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CaBP; 1.
KW Calcium-binding; Zinc; Metal-binding.
FT INIT_MET 0 BY SIMILARITY.
FT CA_BIND 18 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
FT CA_BIND 61 EF-HAND 2 (HIGH AFFINITY) (BY
SIMILARITY).
FT SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 59 DLDA 62

RESULT 8
AAT_METEX
ID AAT_METEX STANDARD; PRT; 93 AA.
AC P52069;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Putative aspartate aminotransferase (EC 2.6.1.1) (Transaminase A)
DE (ASPA) (ORF2) (Fragment).
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IBT 6;
RX MEDLINE=93305286; PubMed=7763712;
RA Valentin H.E., Steinbuechel A.;
RT "Cloning and characterization of the Methylobacterium extorquens
polyhydroxyalkanoic-acid-synthase structural gene.";
RL Appl. Microbiol. Biotechnol. 39:309-317(1993).
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
L-glutamate.

CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
 CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL; L07893; AAA72329.1; -.
 CC HSSP; Q5G232; IBUW.
 CC InterPro; IPR004838; NHtransf_1.
 CC PROSITE; PS00105; AA_TRANSFER_CLASS_1; PARTIAL.
 CC Hypothetical protein; Transferase; Aminotransferase;
 CC Pyridoxal phosphate. 93
 CC NON_TER 93
 CC SEQUENCE 93 AA; 10424 MW; 201376961C632611 CRC64;
 CC -----
 CC Query Match 100.0%; Score 20; DB 1; Length 93;
 CC Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 1 DLDA 4
 CC Db 41 DLDA 44
 CC -----
 CC RESULT 9
 CC S10P_HUMAN STANDARD; PRT; 95 AA.
 CC ID S10P_HUMAN STANDARD; PRT; 95 AA.
 CC AC P25815;
 CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE S-100P protein.
 CC GN S100P OR S100E.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Placenta;
 CC RX MEDLINE=92339442; PubMed=1633809;
 CC RA Becker T., Gerke V., Kube E., Weber K.;
 CC RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
 CC cloning, recombinant protein expression and Ca2+ binding
 CC properties.";
 CC RL Eur. J. Biochem. 207:541-547(1992).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Placenta;
 CC RA Strausberg R.;
 CC RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC RN [3]
 CC RP SEQUENCE OF 1-91.
 CC RC TISSUE=Placenta;
 CC RX MEDLINE=92171935; PubMed=1540168;
 CC RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;
 CC RT "Purification and characterization of a new member of the S-100
 CC protein family from human placenta.";
 CC RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
 CC CC -|- SUBUNIT: Interacts with S100Z.
 CC CC -|- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
 CC CC -|- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL; X65614; CAA46566.1; -.
 CC EMBL; BC006819; AAH06819.1; -.
 CC PIR; S24146; S24146.
 CC HSSP; P02638; 1CFP.
 CC Genew; HGNC:10504; S100P.
 CC MIM; 600614; -.
 CC InterPro; IPR001751; CabP_S100.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; efhand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD003407; CabP_S100; 1.
 CC PROSITE; PS00018; EF_HAND; FALSE_NEG.
 CC PROSITE; PS00303; S100_CABP; 1.
 CC KW Calcium-binding; Placenta.
 CC FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY).
 CC FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).
 CC FT CONFLICT 32 32 E -> T (IN REF. 3).
 CC FT CONFLICT 44 44 F -> E (IN REF. 3).
 CC SQ SEQUENCE 95 AA; 10400 MW; 786E6E3F3EACC6C1 CRC64;
 CC -----
 CC Query Match 100.0%; Score 20; DB 1; Length 95;
 CC Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 1 DLDA 4
 CC Db 60 DLDA 63
 CC -----
 CC RESULT 10
 CC S10Z_HUMAN STANDARD; PRT; 98 AA.
 CC ID S10Z_HUMAN STANDARD; PRT; 98 AA.
 CC AC Q8WXG8;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE S-100Z protein.
 CC GN S100Z.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.; SEQUENCE OF 1-20, SUBUNIT, CALCIUM-BINDING,
 CC TISSUE SPECIFICITY, AND INTERACTION WITH S100P.
 CC RC TISSUE=Prostate;
 CC RX MEDLINE=21614385; PubMed=11747429;
 CC RA Gribenko A.V., Hopper J.E., Makhatadze G.I.;
 CC RT "Molecular characterization and tissue distribution of a novel member
 CC of the S100 family of EF-hand proteins.";
 CC RL Biochemistry 40:15538-15548(2001).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Testis;
 CC RA Strausberg R.;
 CC RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC CC -|- SUBUNIT: Homodimer. Interacts with S100P.
 CC CC -|- TISSUE SPECIFICITY: Highest level of expression in spleen and
 CC leukocytes.
 CC CC -|- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
 CC CC -|- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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CC -----
CC EMBL; AF437876; AAL30893.1; -
CC EMBL; BC022320; AAM22320.1; -
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 1.
CC Pfam; PF01023; S_100; 1.
CC PROSITE; PS00018; EF_HAND; 1.
CC PROSITE; PS00303; S100_CABP; 1.
CC Calcium-binding.
KW INIT_MET 0
FT CA_BIND 19 32 EF-HAND 1 (LOW AFFINITY).
FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).
SQ SEQUENCE 98 AA; 11430 MW; A2053E1809F0F401 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4
| | | |
Db 60 DLDA 63

RESULT 11
SSI_STRGI STANDARD; PRT; 107 AA.
ID P28592;
AC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Alkaline protease inhibitor 2C' (API-2C').
OS Streptomyces griseolincarnatus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=29305;
RN [1]
RP SEQUENCE.
RA Suzuki K., Uyeda M., Shibata M.;
RT "Partial amino acid sequence of an alkaline protease inhibitor, API-2
(b and c).";
RL Agric. Biol. Chem. 45:629-634(1981).
CC -!- FUNCTION: STRONG INHIBITORY ACTIVITY TOWARD SUBTILISIN.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.
CC HSP; P01006; 2SIC.
DR InterPro; IPR00691; Strep_subt_inhib.
DR Pfam; PF00720; SSI; 1.
DR PRINTS; PR00294; SSBTLINHBT.
DR ProDom; PD004028; Strep_subt_inhib; 1.
DR PROSITE; PS00999; SSI; 1.
KW Serine protease inhibitor.
FT DISULFID 29 44 BY SIMILARITY.
FT DISULFID 65 95 BY SIMILARITY.
FT ACT_SITE 67 68 REACTIVE BOND.
SQ SEQUENCE 107 AA; 10972 MW; 76043BA9F876D1CA CRC64;

Query Match 100.0%; Score 20; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4
| | | |
Db 53 DLDA 56

RESULT 12
GLPE_PSEAE STANDARD; PRT; 110 AA.
ID Q915U8;
AC

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiosulfate sulfitransferase glpE (EC 2.8.1.1).
DE GLPE OR PA0589.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Catalyzes, although with low efficiency, the sulfur
transfer reaction from thiosulfate to cyanide (By similarity).
CC -!- CATALYTIC ACTIVITY: Thiosulfate + cyanide -> sulfite + thiocyanate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GLPE FAMILY.
CC -!- SIMILARITY: CONTAINS 1 RHODANSE DOMAIN.
CC -----
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EMBL; AE004495; AAG03978.1; -
DR InterPro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 1.
DR SMART; SM00450; RHOD; 1.
KW Transferase; Glycerol metabolism; Complete proteome.
FT ACT_SITE 65 65 BY SIMILARITY.
SQ SEQUENCE 110 AA; 11963 MW; B0C009A0FDDDFD1FC CRC64;

Query Match 100.0%; Score 20; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4
| | | |
Db 56 DLDA 59

RESULT 13
ALL7_AS PFU STANDARD; PRT; 112 AA.
ID ALL7_AS PFU
AC O42799;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Allergen Asp f 7 (Fragment).
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4202 / AF-102;
RC MEDLINE=98141802; PubMed=9482698;
RA Cramer R.;
RT "Recombinant Aspergillus fumigatus allergens: from the nucleotide
sequences to clinical applications.";

RL Int. Arch. Allergy Immunol. 115:99-114(1998).

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DR EMBL: AJ223315; CAA11255.1; -
KW Allergen.
FT NON_TER 1 1
SQ SEQUENCE 112 AA; 11628 MW; EF64A9B2D4844F6F CRC64;

Query Match 100.0%; Score 20; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 85 DLDA 88

RESULT 14
ID GLNB_CVACA STANDARD; PRT; 113 AA.
AC Q9TM37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nitrogen regulatory protein P-II.
GN GLNB.
OS Cyanidium caldarium.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
CC NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
genome.";
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE
CC GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED
CC CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL
CC ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE
CC EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE
CC DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
CC DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME
CC (BY SIMILARITY).
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P(II) PROTEIN FAMILY.

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DR EMBL: AF022186; AAF13016.1; -
DR HSSP: P05826; 2PII.
DR InterPro: IPR002332; PII_Glnb_UMP.
DR InterPro: IPR002187; PII_glnb.
DR Pfam: PF00543; P-II; 1.
DR PRINTS: PR00340; PIIGLNB.
DR ProDom: PD001194; PII_glnb; 1.
DR PROSITE: PS00496; PII_Glnb_UMP; FALSE_NEG.

DR PROSITE: PS00638; PII_Glnb_CTER; 1.
KW Transcription regulation; Nitrogen fixation; Chloroplast.
FT BINDING 52 52 UMP (BY SIMILARITY).
SQ SEQUENCE 113 AA; 12602 MW; 83C9468B2A3C83BC CRC64;

Query Match 100.0%; Score 20; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 109 DLDA 112

RESULT 15
CH15_DROVI
ID CH15_DROVI STANDARD; PRT; 116 AA.
AC PI3424;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Chorion protein S15.
GN CP15 OR S15.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297142; PubMed=3136055;
RA Martinez-Cruzado J.C., Swimmer C., Fenerjian M.G., Kafatos F.C.;
RT "Evolution of the autosomal chorion locus in Drosophila. I. General
RT organization of the locus and sequence comparisons of genes s15 and
RT s19 in evolutionary distant species.";
RL Genetics 119:663-677(1988).

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DR EMBL: X53421; CAA37501.1; -
DR FIR; S06614; S06614.
DR FlyBase: FBgn0013068; Dvir\Cp15.
KW Chorion.
SQ SEQUENCE 116 AA; 11990 MW; 8FB7E77C87E75777 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 98 DLDA 101

RESULT 16
VATF_HALN1
ID VATF_HALN1 STANDARD; PRT; 120 AA.
AC Q9HNE2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE V-type ATP synthase subunit F (EC 3.6.3.14) (V-type ATPase subunit F).
GN ATPF OR VNG2140G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;

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RN SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -!- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.
CC
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CC
CC EMBL; AE005102; AAG20278.1; -.
CC InterPro; IPR002841; ATPsynth_Fsub.
CC Pfam; PF01990; ATP-synt_F; 1.
CC ProDom; PD003811; ATPsynth_Fsub; 1.
CC Hydrolase; ATP synthesis; Hydrogen ion transport; Complete proteome.
KW SEQUENCE 120 AA; 12388 MW; 9A88D7D7FF21631 CRC64;
Query Match 100.0%; Score 20; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
DB 36 DLDA 39
RESULT 17
YEBF_ECOLI
ID YEBF_ECOLI STANDARD; PRT; 122 AA.
AC P32119;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein yebf precursor.
GN YEBF OR B1847.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
OX [1]
RN SEQUENCE FROM N.A.
RP Smith J.M., Nygaard P.;
RA STRAIN-K12;
RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3]
RN SEQUENCE FROM N.A.

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RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takenoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (potential).
CC
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CC
CC EMBL; L20897; AAA23859.1; -.
CC EMBL; AE000278; AAC74917.1; -.
CC EMBL; D90827; BAA15653.1; -.
CC Ecogene; EGI1807; yebf.
CC DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC KW Hypothetical protein; Membrane; Lipoprotein; Signal;
CC Complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 122 HYPOTHETICAL LIPOPROTEIN YEBF.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 122 AA; 13464 MW; EC941612C666BE88 CRC64;
Query Match 100.0%; Score 20; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
DB 41 DLDA 44
RESULT 18
RNPA_STRBI
ID RNPA_STRBI STANDARD; PRT; 123 AA.
AC P25817;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
DE P protein) (Protein C5).
DE RNPA.
OS Streptomyces bikiniensis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1896;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN-Var. Zorbonensis;
RX MEDLINE=92354937; PubMed=1379566;
RA Morse D.P., Schmidt F.J.;
RT "Sequences encoding the protein and RNA components of ribonuclease P
RL from Streptomyces bikiniensis var. zorbonensis.";
RL Gene 117:61-66(1992).
CC -!- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5' terminus. It can also
CC cleave other RNA substrates such as 4.5S RNA. The protein
CC component plays an auxiliary but essential role in vivo by binding
CC to the 5'-leader sequence and broadening the substrate specificity
CC of the ribozyme.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.

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CC of the ribozyme (By similarity).
CC -! CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.
CC -! SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (By similarity).
CC -! SIMILARITY: BELONGS TO THE RNPA FAMILY.
CC -----
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CC -----
DR EMBL: AF187159; AAA26732.1; -
DR EMBL: AL049826; CABA2696.1; -
DR InterPro: IPR000100; Ribonuclease_P.
DR Pfam: PF00825; Ribonuclease_P; 1.
DR TIGRFAMs: TIGR00188; rnpA; 1.
DR PROSITE: PS00648; RIBONUCLEASE_P; 1.
DR Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
KW Complete proteome.
KW SEQUENCE 123 AA; 13320 MW; 0D4D4E26A20B6C39 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 109 DLDA 112

RESULT 20
VG19_BPMD2 STANDARD; PRT; 124 AA.
ID AC
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 19 protein (GPI9).
GN 19.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC unclassified Siphoviridae.
OX NCBI_TaxID=283369;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: Implications for phage
RT evolution.;"
RL J. Mol. Biol. 279:143-164 (1998).
CC -----
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CC -----
DR EMBL: AF022214; AAC18459.1; -
DR SEQUENCE 124 AA; 14135 MW; F85A03C16A742837 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 42 DLDA 45

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RESULT 21
CCDP_MAIZE          STANDARD;          PRT;      129 AA.
AC   Q01595;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DE   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Cortical cell delineating protein precursor (Root-specific protein
DE   ZRP3).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A. TISSUE=Root;
RC   STRAIN=CV. NKH31; TISSUE=Root;
RX   MEDLINE=9309234; PubMed=1463822;
RA   John I., Wang H., Held B.M., Wurtele E.S., Colbert J.T.;
RA   "An mRNA that specifically accumulates in maize roots delineates a
RA   novel subset of developing cortical cells.";
RL   Plant Mol. Biol. 20:821-831(1992).
CC   -!- FUNCTION: DELINEATES A NOVEL SUBSET OF DEVELOPING CORTICAL CELLS.
CC   IT IS PROBABLY INVOLVED IN SOME ASPECT OF TRANSPORT OF MOLECULES
CC   TO OR FROM THE VASCULATURE.
CC   -!- TISSUE SPECIFICITY: CORTICAL GROUND MERISTEM OF DEVELOPING ROOTS.
CC   -!- SIMILARITY: STRONG; TO CARROT DC2.15 AND PEMB3.
CC   -----
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CC   -----
CC   EMBL; Z12103; CAA78088.1; -.
CC   DR   PIR: S28009; S28009.
CC   DR   HSSP: P24337; LHP.
CC   DR   MaizeDB; 65581; -.
CC   DR   InterPro; IPR003612; AAI.
CC   DR   InterPro; IPR001768; TRY/AMYL_INHPT.
CC   DR   Pfam; PF00234; tryp_alpha_amy1; 1.
CC   DR   SMART; SM00499; AAI; 1.
CC   DR   SMART; SM00499; AAI; 1.
CC   KW   Signal; Glycoprotein; Repeat.
CC   FT   SIGNAL          1..19
CC   FT   CHAIN           1..19
CC   FT   CARBOHYD        25..25
CC   FT   DOMAIN          29..40
CC   FT   REPEAT          29..34
CC   FT   REPEAT          35..40
CC   SQ   SEQUENCE 129 AA; 13526 MW; 39AAE618761D948B CRC64;
Query Match      100.0%; Score 20; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DLDA 4
Db   84 DLDA 87
RESULT 22
Y4IP_RHISN
ID   Y4IP_RHISN          STANDARD;          PRT;      131 AA.
AC   P55499;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Hypothetical 14.4 kDa protein Y4IP.
GN   Y4IP.
OS   Rhizobium sp. (strain NGR234).
OG   Plasmid sym NGR234a.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=394;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97305956; PubMed=9163424;
RA   Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA   Perret X.;
RA   "Molecular basis of symbiosis between Rhizobium and legumes.";
RL   Nature 387:394-401(1997).
CC   -!- SIMILARITY: NONE OBVIOUS EXCEPT FOR SIMILARITY TO N-TERMINAL
CC   OF PUTATIVE TRANSPOSASE Y4RJ. POTENTIAL FRAGMENT.
CC   -----
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CC   -----
CC   EMBL; AE000079; AAB91711.1; -.
CC   DR   Hypothetical protein; Plasmid.
CC   SQ   SEQUENCE 131 AA; 14387 MW; 9F2AE3B1FC6EC6CF CRC64;
Query Match      100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 DLDA 4
Db   15 DLDA 18
RESULT 23
RNK_ECOLI
ID   RNK_ECOLI          STANDARD;          PRT;      136 AA.
AC   P40679;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of nucleoside diphosphate kinase.
GN   RNK OR B0610 OR Z0754 OR ECS0649.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96015444; PubMed=7565093;
RA   Schlittman D., Shankar S., Chakrabarty A.M.;
RA   "The Escherichia coli genes ssrA and rnk can functionally replace the
RA   Pseudomonas aeruginosa alginate regulatory gene algR2.";
RL   Mol. Microbiol. 16:309-320(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RA   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA   Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA   Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RA   Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL
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[4]
RN SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horluchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
[5]
RN SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouisis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
[6]
RN SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE=21152331; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC ALGINATE REGULATORY GENE ALGR2.
CC -----
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CC -----
DR EMBL; L37900; AAC36933.1; -;
DR EMBL; AE000166; AAC73711.1; -;
DR EMBL; U82598; AAB40810.1; -;
DR EMBL; D90701; BAA35239.1; -;
DR EMBL; D90702; BAA35248.1; -;
DR EMBL; AE005240; AAG54945.1; -;
DR EMBL; AP002552; BAB34072.1; -;
DR Ecogene; EGI2637; rnk.
KW Complete proteome.
SQ SEQUENCE 136 AA; 14927 MW; 7043926623BA5E1E CRC64;
Query Match 100.08; Score 20; DB 1; Length 136;
Best Local Similarity 100.08; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DLDA 4
| | | |
Db 10 DLDA 13
RESULT 24
INL2_DROME
ID INL2_DROME STANDARD; PRT; 137 AA.
AC Q9VT51;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT DE
DE Probable insulin-like peptide 2 precursor (Insulin-related peptide).
GN IRP OR CG8167.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21107400; PubMed=11179818;
RT Vanden Broeck J.;
RT "Neuropeptides and their precursors in the fruitfly, Drosophila
RT melanogaster";
RL Peptides 22:241-254(2001).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ291726; CAC17605.1; -;
DR EMBL; AE003550; AAF50204.1; -;
DR HSSP; P01344; IGF2.
DR FlyBase; FBgn0036046; IRP.
DR InterPro; IPR004825; Ins/IGF/relax.

```

DR InterPro: IPR001469; ATPSynt_DE.
DR Pfam: PF00401; ATP-synt_DE. 1.
DR Pfam: PF02823; ATP-synt_DE.N; 1.
DR Pfam: PF000944; ATPSynt_DE; 1.
DR TIGRFAMs: TIGR01216; ATP_synt_epsilon; 1.
DR KW Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
KW Complete proteome.
SQ SEQUENCE 140 AA; 15246 MW; 8D71A8A16566EC9D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
    ||||
DB 90 DLDA 93

RESULT 26
Y4JK_RHISN STANDARD; PRT; 140 AA.
ID Y4JK_RHISN
AC P55511;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative plasmid stability protein Y4JK.
DE Y4JK.
GN Rhizobium sp. (strain NGR234).
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
RN [1]
RX MEDLINE=97305956; Pubmed=9163424;
RA Freiberger C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- FUNCTION: INVOLVED IN PLASMID STABILITY (POTENTIAL).
CC -!- SIMILARITY: STRONG, TO P.SYRINGAE (PV. TOMATO) PLASMID STABILITY
CC PROTEIN STTB. ALSO STRONG, TO A N.GONORRHOEA ORF CAPABLE OF
CC INHIBITING GONOCOCCAL TRANSFORMATION (PGCU22).
CC -----
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CC -----
CC EMBL; AE000080; AAB91723.1; -.
DR InterPro: IPR002716; PIN.
DR Pfam: PF01850; PIN; 1.
DR KW Hypothetical protein; Plasmid.
SQ SEQUENCE 140 AA; 15119 MW; 9142E3F8C2BFCD0C CRC64;

Query Match 100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
    ||||
DB 79 DLDA 82

RESULT 27
YK24_PSEAE
ID YK24_PSEAE STANDARD; PRT; 140 AA.
AC P23205; O91290;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PA2024.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
[1]
SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 405:959-964(2000).
[2]
SEQUENCE OF 1-28 FROM N.A.
RC STRAIN-PA08;
RX MEDLINE=91194546; PubMed=1849605;
RA Perry A.C.F., Ni Bhriain N., Brown N.L., Rouch D.A.;
RT "Molecular characterization of the gor gene encoding glutathione
reductase from Pseudomonas aeruginosa: determinants of substrate
specificity among pyridine nucleotide-disulphide oxidoreductases.";
RL Mol. Microbiol. 5:163-171(1991).
CC -----
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CC -----
CC EMBL; AE004629; AAG05412.1; -
DR EMBL; X54201; CAA38121.1; -
DR PIR; S15235; S15235.
DR InterPro; IPR004360; Gly_bleo_diox.
DR Pfam; PF00903; Glyoxalase; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 140 AA; 15373 MW; 26221B19B328F38 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIDA 4
Db 14 DLDA 17

RESULT 28
DTD_STRCO
ID DTD_STRCO STANDARD; PRT; 141 AA.
AC Q9K4F6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-).
GN DTD OR SC04182 OR SC066.19C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)." ;
RL Nature 411:141-147(2002).
CC -!- FUNCTION: Hydrolyzes D-tyrosyl-tRNA(Tyr) into D-tyrosine and free
CC tRNA(Tyr). Could be a defense mechanism against a harmful effect
CC of D-tyrosine (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE DTD FAMILY.
CC -----
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CC -----
CC EMBL; AL358692; CAB94086.1; -
DR HSP; P32147; 1JKE.
DR InterPro; IPR003732; DUF154.
DR Pfam; PF02580; DUF154; 1.
DR TIGRFAMs; TIGR00256; TIGR00256; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 141 AA; 14968 MW; 55F42ECAAF299E37 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 64 DLDA 67

RESULT 29
HBA3_XENLA
ID HBA3_XENLA STANDARD; PRT; 141 AA.
AC P06636;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha-3 chain (Alpha-T3).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297748; PubMed=2993998;
RA Banville D., Williams J.G.;
RT "The pattern of expression of the Xenopus laevis tadpole alpha-globin
RT genes and the amino acid sequence of the three major tadpole alpha-
RT globin polypeptides.";
RL Nucleic Acids Res. 13:5407-5421(1985).
CC -!- FUNCTION: THIS IS A LARVAL (TADPOLE) ALPHA-GLOBIN.
CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
CC -!- TISSUE SPECIFICITY: Red blood cells.
CC -!- POLYMORPHISM: ALPHA T3 MAY BE AN ALLELE OF ALPHA T4.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC -----
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DR EMBL: X02796; CAA26564.1; -
DR PIR: A24338; A24338.
DR HSP: P01922; IABW.
DR InterPro: IPR002338; Alpha_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00612; ALPHAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte.
FT INIT_MET 0
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15303 MW; F0F1694366B7C0A7 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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|
|
Db 75 DLDA 78

RESULT 30
HBA3_XENTR STANDARD; PRT; 141 AA.
AC P08422;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha-3 chain (Larval).
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xenopodinae; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88157727; PubMed=3347501;
RA Koechel W., Fianne K., Beck J., Meyerhof W.;
RA "Nucleotide sequence of a larval alpha globin gene from Xenopus
RA tropicalis."
RL Nucleic Acids Res. 16:1625-1625(1988).
CC -!- FUNCTION: THIS IS A LARVAL (TADPOLE) ALPHA-GLOBIN.
CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
CC -!- TISSUE SPECIFICITY: Red blood cells.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: X06664; CAA29864.1; -
DR PIR: A28538; A28538.
DR HSP: P01966; 1FSX.
DR InterPro: IPR002338; Alpha_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00612; ALPHAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte.
FT INIT_MET 0
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15355 MW; 01C7C9F83973FCDA CRC64;

Query Match 100.0%; Score 20; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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|
|
Db 75 DLDA 78

RESULT 31
MMS5_MYCTU STANDARD; PRT; 142 AA.
AC O53785;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative membrane protein MMP5.
GN MMP5 OR RV0677C OR MT0706 OR MTV040.05C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RA complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RA laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE MP5 FAMILY.

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DR EMBL: AL021943; CAA17460.1; -
DR EMBL: AE006964; AAK44931.1; -
DR TIGR: MT0706; -
DR TubercuList; RV0677c; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 25 POTENTIAL.
SQ SEQUENCE 142 AA; 15248 MW; 055BD99A3F46E8F5 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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|

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Db 73 DLDA 76

RESULT 32
RL1L_STRAT
ID RL1L_STRAT STANDARD; PRT; 144 AA.
AC 087085;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1890;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14888;
RX MEDLINE=98401489; PubMed=9731302;
RA Kawamoto S., Ochi K.;
RT "Comparative ribosomal protein (L11 and L30) sequence analyses of
several Streptomyces spp. commonly used in genetic studies.";
RL Int. J. Syst. Bacteriol. 48:597-600(1998).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
(BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AB005914; BAA31981.1; -
DR HSSP; P29395; IMMS.
DR InterPro; IPR000911; Ribosomal_L11.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding.
FT Ribosomal protein; RNA-binding.
FT VARIANT 28 31 MISSING (IN THIOPEPTIN RESISTANCE).
SQ SEQUENCE 144 AA; 15232 MW; 7820A6BCC9B45EA3 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
| | | |
DB 123 DLDA 126

RESULT 33
RL1L_STRGR
ID RL1L_STRGR STANDARD; PRT; 144 AA.
AC P36258; O32448;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK OR RELC.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=94314177; PubMed=8039667;
RA Kuberski S., Kasberg T., Distler J.;
RT "The nusG gene of Streptomyces griseus: cloning of the gene and

analysis of the A-factor binding properties of the gene product.";
FEMS Microbiol. Lett. 119:33-39(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 13189;
RX MEDLINE=97464644; PubMed=9323358;
RA Kawamoto S., Zhang D., Ochi K.;
RT "Molecular analysis of the ribosomal L11 protein gene (rplK - relC)
of Streptomyces griseus and identification of a deletion allele.";
Mol. Gen. Genet. 255:549-560(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
(BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; X72787; CAA51297.1; -
DR EMBL; D87846; BAA22444.1; -
DR EMBL; D87846; BAA22445.1; -
DR PIR; S32235; S32235.
DR HSSP; P29395; IMMS.
DR InterPro; IPR000911; Ribosomal_L11.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding; Antibiotic resistance.
FT VARIANT 28 31 MISSING (IN THIOPEPTIN RESISTANCE).
SQ SEQUENCE 144 AA; 15032 MW; D70E8D7FDCD68122 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
| | | |
DB 123 DLDA 126

RESULT 34
RL1L_STRSQ
ID RL1L_STRSQ STANDARD; PRT; 144 AA.
AC Q07975;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK.
OS Streptomyces sp. (strain FRI-5).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93281414; PubMed=8506151;
RA Ruengjitchachawalya M., Okamoto S., Nihira T., Yamada M.;
RT "Nucleotide sequence of the genes encoding L11 and L1 equivalent
ribosomal protein from Streptomyces sp. FRI-5.";
Nucleic Acids Res. 21:2524-2524(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
(BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: D14451; BAA03346.1; -;
DR PIR: S40772; S40772.
DR HSP: P29395; LMWS.
DR InterPro: IPR000911; Ribosomal_L11.
DR Pfam: PF00298; Ribosomal_L11; 1.
DR ProDom: PD001367; Ribosomal_L11; 1.
DR PROSITE: PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding.
SQ SEQUENCE 144 AA; 15328 MW; A65FBB987D202E6 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 123 DLDA 126

RESULT 35
RBFA_RHILLO
ID RBFA_RHILLO STANDARD; PRT; 146 AA.
AC Q98BI7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-binding factor A.
GN RBFA OR MLR5557.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;

CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=MAFF303099;
CC MEDLINE=21082930; PubMed=11214968;
CC Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
CC Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
CC Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
CC Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
CC Takeuchi C., Yamada M., Tabata S.;
CC "Complete genome structure of the nitrogen-fixing symbiotic bacterium
CC Mesorhizobium loti";
CC DNA Res. 7:331-338(2000).
CC -1- FUNCTION: Associates with free 30S ribosomal subunits (but not
CC with 30S subunits that are part of 70S ribosomes or polysomes).
CC Essential for efficient processing of 16S rRNA. May interact with
CC the 5'terminal helix region of 16S rRNA (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RBFA FAMILY.

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CC EMBL: AP003006; BAB51985.1; -;
DR InterPro: IPR000238; Rib_bind_factA.
DR Pfam: PF02033; RBFA; 1.
DR ProDom: PD007327; Rib_bind_factA; 1.
DR TIGRFAMs: TIGR00082; rbfa; 1.
DR PROSITE: PS01319; RBFA; 1.
KW rRNA processing; Complete proteome.
SQ SEQUENCE 146 AA; 16416 MW; 3E114115F74CEFA7 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DLDA 4
||||
Db 126 DLDA 129

RESULT 36
GLBP_CHITH
ID GLBP_CHITH STANDARD; PRT; 152 AA.
AC P11582;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Globin CTT-E/E' precursor.
GN CTT-E AND CTT-E'.
OS Chironomus thummi thummi (Midge).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7155;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056313; PubMed=3678833;
RA Antoine M., Erbil C., Muench E., Schnell S., Niessing J.;
RT "Genomic organization and primary structure of five homologous pairs
RT of intron-less genes encoding secretory globins from the insect
RT Chironomus thummi thummi.";
RL Gene 56:41-51(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Hankeln T., Amid C., Weich B., Schmidt E.R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC EMBL: M17604; AAA28253.1; -;
DR EMBL: M17695; AAA28258.1; -;
DR EMBL: Y10622; CAA71643.1; -;
DR HSP: P02229; LECA
DR InterPro: IPR002336; Erythcrurin.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00611; ERYTHCRURIN.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Signal.
FT SIGNAL 1 15
FT CHAIN 16 152 GLOBIN CTT-E/E'.
FT METAL 73 73 IRON (HEME DISTAL LIGAND)
FT FT (BY SIMILARITY).
FT METAL 102 102 IRON (HEME PROXIMAL LIGAND)
FT FT (BY SIMILARITY).
SQ SEQUENCE 152 AA; 15964 MW; 52D70B8CF57CFA9E CRC64;

Query Match 100.0%; Score 20; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
||||
Db 60 DLDA 63

RESULT 37
RS15_ARATH
ID RS15_ARATH STANDARD; PRT; 152 AA.

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_194.
GN AQ_194.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus";
RL Nature 392:353-358(1998).
CC -----
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CC -----
DR EMBL; AE000677; AAC06532.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 154 AA; 18089 MW; 0FCF78184C85ADC5 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDA 4
|||||
Db 126 DIDA 129

RESULT 40
DUT_CAUCR STANDARD; PRT; 155 AA.
AC Q9A253;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
DE (dUTPase) (dUTP pyrophosphatase).
GN DUT OR CC3713.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- FUNCTION: This enzyme is involved in nucleotide metabolism: it
CC produces dUMP, the immediate precursor of thymidine nucleotides
CC and it decreases the intracellular concentration of dUTP so that
CC uracil cannot be incorporated into DNA (By similarity).
CC -!- CATALYTIC ACTIVITY: dUTP + H(2)O = dUMP + diphosphate.

CC -!- PATHWAY: De novo synthesis of thymidylate.
CC -!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
CC -----
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CC -----
DR EMBL; AE000629; AAK25675.1; -
DR HSSP; P06968; 1EUW.
DR TIGR; CC3713; -
DR InterPro; IPR001428; DeoxyUTPase.
DR Pfam; PF00692; dUTPase; 1.
DR ProDom; PD000946; DeoxyUTPase; 1.
DR TIGRFAMs; TIGR00576; dut; 1.
KW Hydrolase; Nucleotide metabolism; Complete proteome.
SQ SEQUENCE 155 AA; 16215 MW; 534EC085942C4118 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIDA 4
|||||
Db 139 DIDA 142

RESULT 41
YS51_MYCTU STANDARD; PRT; 156 AA.
AC O05808;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2851c.
GN RV2851c OR MT2917 OR MTCY24A1.06.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.
CC -----
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DR EMBL; Z95207; CAB08455.1; -
DR EMBL; AE007116; AAK47243.1; -
DR TIGR; MT2917; -
DR Tuberculin; Rv2851c; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 156 AA; 17670 MW; 6ECBAE9F33FB365E CRC64;

Query Match 100.0%; Score 20; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
DB 12 DLDA 15

RESULT 42

YE19_MYCTU STANDARD; PRT; 157 AA.
AC P71688;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein Rv1419.
GN Rv1419 OR MT1462 OR MTCY21B4.37.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OshKosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.

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CC EMBL; Z80108; CAB02167.1; -
DR EMBL; AE007017; AAK45727.1; -

DR TIGR; MT1462; -
DR Tuberculin; Rv1419; -
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS0231; RICIN_B_LECTIN; 1.
KW Hypothetical protein; Transmembrane; Lectin; Complete proteome.
FT TRANSMEM 6 26 POTENTIAL.
FT DOMAIN 33 157 RICIN B-TYPE LECTIN.
SQ SEQUENCE 157 AA; 16853 MW; 35CB2E952788773D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
DB 122 DLDA 125

RESULT 43

ATPX_SYNP6 STANDARD; PRT; 158 AA.
AC P08446;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase B' chain (EC 3.6.3.14) (Subunit II).
GN ATPG.
OS Synecococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87311713; PubMed=3041005;
RA Cozens A.L., Walker J.E.;
RT "The organization and sequence of the genes for ATP synthase subunits
RT in the cyanobacterium Synecococcus 6301. Support for an
RT endosymbiotic origin of chloroplasts."
RL J. Mol. Biol. 194:359-383(1987).
CC -1- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM OF
CC B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) -> ADP + phosphate +
CC H(+)(Out).
CC -1- SUBUNIT: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF0) SUBUNIT OF THE ATPASE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.

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DR EMBL; X05302; CAA28925.1; -
DR PIR; S10828; LWVCBB.
DR InterPro; IPR002146; ATPsynth_B/B'sub.
DR Pfam; PF00430; ATP-synt_B; 1.
KW Hydrogen ion transport; Transmembrane; CF(0).
SQ SEQUENCE 158 AA; 17412 MW; 60A5896390DC28E0 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
DB 21 DLDA 24

RESULT 44

ATPX_ANASP STANDARD; PRT; 163 AA.
AC P12410;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase B' chain (EC 3.6.3.14) (Subunit II).
GN ATPG OR ALL0008.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88298650; PubMed=2900236;
RA McCarr D.F., Whitaker R.A., Alam J., Vrba J.M., Curtis S.E.;
RT "Genes encoding the alpha, gamma, delta, and four F0 subunits of ATP synthase constitute an operon in the cyanobacterium Anabaena sp. strain PCC 7120.";
RT strain PCC 7120.";
RL J. Bacteriol. 170:3448-3458(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimp S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM OF B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).
CC -!- SUBUNIT: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
CC -!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; AF242564; AAA21988.1; -;
DR EMBL; AF003581; BAB77532.1; -;
DR PIR; D31090; D31090.
DR InterPro; IPR002146; ATPsynt_B/B' sub.
DR Pfam; PF00430; ATP-synt_B; 1.
KW Hydrogen ion transport; Transmembrane; CF(0); Complete proteome.
SQ SEQUENCE 163 AA; 17972 MW; E48D1D0F9C4BA705 CRC64;
Query Match 100.0%; Score 20; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 21 DLDA 24
RESULT 45
FUSE_BURCE STANDARD; PRT; 168 AA.
AC P24130;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Fusaric acid resistance protein|fuse.
GN FUSE.
OS Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UK1;
RX MEDLINE=92109974; PubMed=1370369;
RA Utsumi R., Yagi T., Katayama S., Katsuragi K., Tachibana K.,
RA Toyoda H., Ouchi S., Obata K., Shibano Y., Noda M.;
RT "Molecular cloning and characterization of the fusaric acid-resistance gene from Pseudomonas cepacia.";
RL Agric. Biol. Chem. 55:1913-1918(1991).
CC -!- FUNCTION: INVOLVED IN THE RESISTANCE (DETOXIFICATION) OF THE FUNGAL TOXIN FUSARIC ACID.
CC -----
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CC -----
DR EMBL; S77489; AAC60392.1; -;
DR EMBL; D12503; BAA02068.1; -;
DR PIR; JS0513; JS0513.
SQ SEQUENCE 168 AA; 18484 MW; 5197296234AFBA5E CRC64;
Query Match 100.0%; Score 20; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLDA 4
Db 35 DLDA 38
Search completed: February 6, 2003, 11:16:44
Job time : 7.33333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 21.3333 Seconds
(without alignments)
38.634 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4211

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	20	100.0	30	17	Q8ZVL0		Q8ZVL0 pyrobaculum
2	20	100.0	31	2	Q9S5Z5		Q9S5Z5 streptomyces
3	20	100.0	48	4	Q75253		Q75253 homo sapien
4	20	100.0	49	2	Q8RMK4		Q8RMK4 corynebacte
5	20	100.0	51	5	Q26905		Q26905 trichostro
6	20	100.0	54	12	Q99175		Q99175 porcine ent
7	20	100.0	55	2	Q9XC71		Q9XC71 salmonella
8	20	100.0	55	12	Q64995		Q64995 eastern equ
9	20	100.0	56	10	Q9M615		Q9M615 vitis ripar
10	20	100.0	60	17	Q8ZVG7		Q8ZVG7 pyrobaculum
11	20	100.0	61	16	Q53965		Q53965 streptomyces
12	20	100.0	62	16	Q9ZS16		Q9ZS16 rhizobium m
13	20	100.0	63	10	Q9SPN4		Q9SPN4 oryza sativ
14	20	100.0	65	2	Q54732		Q54732 synchococc
15	20	100.0	66	16	O50486		O50486 streptomyces
16	20	100.0	67	2	Q9L8X2		Q9L8X2 streptomyces

ALIGNMENTS

RESULT 1

Q8ZVL0 PRELIMINARY; PRT; 30 AA.
 AC Q8ZVL0;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE PaREP2b.
 GN PAE2231.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 aerophilum";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 DR EMBL; AE009864; AAL64046.1; -
 KW Complete proteome.
 SQ SEQUENCE 30 AA; 3535 MW; 16301757DB3B1468 CRC64;

Query Match 100.0%; Score 20; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
 Db 7 DLDA 10
 ||||

RESULT 2

Q9S5Z5 PRELIMINARY; PRT; 31 AA.
 ID Q9S5Z5
 AC Q9S5Z5;

Q918x0 streptomyces
 Q9KIL3 streptomyces
 Q9CIA6 lactococcus
 Q9RL16 bos taurus
 Q9LD48 arbidopsis
 Q92K57 rhizobium m
 Q92S57 rhizobium m
 Q92S57 rhizobium m
 Q9YW97 epiphyas po
 Q9YD33 streptococci
 Q9FBC6 streptococci
 Q99Q96 streptomyces
 Q93EG1 helicobacte
 P79246 sus scrofa
 P93274 malus domes
 Q95323 vaccinia vi
 Q98040 shope fibro
 Q90Y04 poephila gu
 Q96536 streptomyces
 Q9AN31 bradyrhizob
 Q9F7T4 streptococci
 Q92NC0 rhizobium m
 Q9AZ98 lactobacilli
 Q93449 helicobacte
 Q92L89 helicobacte
 Q9A5F8 caulobacter
 Q9A0C1 streptococci
 Q926P1 listeria in
 Q91B27 chesapeake

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DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE RNase P protein (Fragment).
GN RNPA.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3A(2);
RA Cal-Mor O., Borovok I., Cohen G., Aharonowitz Y.;
RT "Gene organization in the trxB/A/oriC region of the Streptomyces
RL coelicolor 3A(2) chromosome and comparison with other bacteria.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031590; AAC03489.1; -;
FT NON_TER 1
SQ SEQUENCE 31 AA; 3069 MW; 709BE4DA5CAA86E5 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 17 DLDA 20

RESULT 3
ID 075253 PRELIMINARY; PRT; 48 AA.
AC 075253;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE R31341_2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carraro A.V.;
RT "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
RL serine protease gene cluster.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005331; AAC27666.1; -;
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PROSITE; PS50102; RRM; 1.
FT NON_TER 48
SQ SEQUENCE 48 AA; 5689 MW; 98DF39514911566A CRC64;

Query Match 100.0%; Score 20; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 3 DLDA 6

RESULT 4
ID Q8RMK4 PRELIMINARY; PRT; 49 AA.
Q8RMK4

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AC Q8RMK4;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ORF1.
OS Corynebacterium diphtheriae.
OG Plasmid pNG2.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S601;
RA Tauch A., Bischoff N., Kalinowski J., Puehler A.;
RT "Insights into the genetic organization of the Corynebacterium
RT diphtheriae erythromycin resistance plasmid pNG2 deduced from its
RT complete nucleotide sequence.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492560; AAM12761.1; -;
KW Plasmid.
SQ SEQUENCE 49 AA; 5396 MW; E4F2A47F4DB7C895 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 15 DLDA 18

RESULT 5
ID Q26905 PRELIMINARY; PRT; 51 AA.
AC Q26905;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Beta-tubulin (Fragment).
GN TCB-1.
OS Trichostrongylus colubriformis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Trichostrongylidae; Trichostrongylinae;
OC Trichostrongylus.
OX NCBI_TaxID=6319;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCMASTER;
RA Grant W.N., Mascord L.J.;
RT "Beta-tubulin gene polymorphism and benzimidazole resistance in
RT Trichostrongylus colubriformis.";
RL Int. J. Parasitol. 0:0-0(1995).
DR EMBL; U39620; AAA80231.1; -;
DR InterPro; IPR003008; Tubulin_Ftsz.
DR Pfam; PF00091; tubulin; 1.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 51 AA; 5750 MW; 78003D1CD26CE60B CRC64;

Query Match 100.0%; Score 20; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 38 DLDA 41

RESULT 6
ID Q99I75 PRELIMINARY; PRT; 54 AA.
Q99I75
AC Q99I75;

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DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Capsid VP2 (Fragment).
DE 1B.
OS Porcine enterovirus 10.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=106967;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LF54;
RX MEDLINE=21102978; PubMed=11161281;
RA Kaku Y., Sarai A., Murakami Y.;
RT "Genetic reclassification of porcine enteroviruses.";
RL J. Gen. Virol. 82:417-424(2001).
DR EMBL; AB049562; BAB32827.1; -.
DR HSSP; P12915; IBEV.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
FT NON_TER 1
FT NON_TER 54
SQ SEQUENCE 54 AA; 5655 MW; EC728F3DC4595BB7 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 44 DLDA 47

RESULT 7
Q9XC71
ID Q9XC71 PRELIMINARY; PRT; 55 AA.
AC Q9XC71;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Aminopeptidase N (Fragment).
GN PEPN.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Norel F., Coyault C., Bossi L., Figueroa-Bossi N.;
RT "Attachment sites of Gifsy-1 and Gifsy-2 prophages in the Salmonella typhimurium chromosome.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF147699; AAD43091.1; -.
DR MEROPS; M01.005; -.
FT NON_TER 55
SQ SEQUENCE 55 AA; 6257 MW; 7C4F369F417345A3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 28 DLDA 31

RESULT 8
Q64995
ID Q64995 PRELIMINARY; PRT; 55 AA.
AC Q64995;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Eastern equine encephalomyelitis virus (South American strain) RNA 5'
DE terminal sequence (Fragment).
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis
OS virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83010261; PubMed=6288962;
RA Ou J.-H., Trent D.W., Strauss J.H.;
RT "The 5'-non-coding regions of alphavirus RNAs contain repeating
RT sequences.";
RL J. Mol. Biol. 156:719-730(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83268700; PubMed=6308269;
RA Ou J.-H., Strauss E.G., Strauss J.H.;
RT "The 5' terminal sequences of the genomic RNAs of several
RT alphaviruses.";
RL J. Mol. Biol. 168:1-15(1983).
DR EMBL; K00701; AAA42982.1; -.
FT NON_TER 55
SQ SEQUENCE 55 AA; 6227 MW; C9E12ADDB190BCB3 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 7 DLDA 10

RESULT 9
Q9M615
ID Q9M615 PRELIMINARY; PRT; 56 AA.
AC Q9M615;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Proline rich protein 2 (Fragment).
GN PRP2.
OS Vitis riparia (Frost grape) (Vitis vulpina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=96939;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER BUDS;
RA Li X.Z., McKersie B.D.;
RT "Freezing tolerance in grapevines.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF220197; AAF32353.1; -.
DR HSSP; P24337; 1HVP.
DR InterPro; IPR001768; Try/amyl_inhbr.
DR Pfam; PF00234; tryp_alpha_amyl; 1.
FT NON_TER 1
SQ SEQUENCE 56 AA; 5737 MW; D3E02C9CB5FC8ECE CRC64;

Query Match 100.0%; Score 20; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 12 DLDA 15

RESULT 10
Q8ZVG7
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ID O8ZVG7 PRELIMINARY; PRT; 60 AA.
AC O8ZVG7;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein PAE2291.
GN PAE2291.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009868; AAL64089.1; -.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 60 AA; 6575 MW; 3872131892320B6D CRC64;

Query Match 100.0%; Score 20; DB 17; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 16 DLDA 19

RESULT 11
Q53965 PRELIMINARY; PRT; 61 AA.
ID Q53965;
AC Q53965;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE EXCISTONASE.
GN XIS OR SCO4616 OR SCD39.16C.
OS Streptomyces coelicolor.
OG Plasmid pRI1724.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=PRI1724;
RX MEDLINE=93259953; PubMed=8387993;
RA Brasch M.A., Pettis G.S., Lee S.C., Cohen S.N.;
RT "Localization and nucleotide sequences of genes mediating site-
RT specific recombination of the SLP1 element in Streptomyces lividans."
RL J. Bacteriol. 175:3067-3074(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
```

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RL Mol. Microbiol. 21:77-96(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; X71358; CAA50493.1; -.
DR EMBL; AL392146; CAC08269.1; -.
KW Plasmid.
SQ SEQUENCE 61 AA; 7103 MW; CCC67B2F0D173512 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 61;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 49 DLDA 52

RESULT 12
Q92S16 PRELIMINARY; PRT; 62 AA.
ID Q92S16;
AC Q92S16;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical unknown protein SMC02319.
GN R00625 OR SMC02319.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Bountry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591784; CAC45197.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 62 AA; 7001 MW; F5F3E902AD9E669F CRC64;

Query Match 100.0%; Score 20; DB 16; Length 62;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 55 DLDA 58

RESULT 13
Q9SPN4 PRELIMINARY; PRT; 63 AA.
ID Q9SPN4;
AC Q9SPN4;
RT 01-MAY-2000 (TRENBLrel. 13, Created)
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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 6.5 kDa protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. IR-BB21;
RA Han F., Kilian A., Chen J.P., Kudrna D., Steffenson B., Yamamoto K.,
RA Matsumoto T., Sasaki T., Kleinohs A.;
RT "Sequence analysis of a rice BAC covering the syntenous barley Rpg1
region.";
RL Genome 0.0-0.0(1999).
DR EMBL; AF149815; AAF00148.1; -.
DR HSSP; P24337; IHYP.
DR InterPro; IPR001768; Try/amyl_inhtr.
DR Pfam; PF00234; tryp_alpha_amyl; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 63 AA; 6506 MW; 81BA557A94EF695D CRC64;

Query Match 100.0%; Score 20; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 19 DLDA 22

RESULT 14
Q54732 PRELIMINARY; PRT; 65 AA.
AC Q54732;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE Synchococcus PCC7942 chromosomal region used as basis of neutral site
DE II recombinational cloning vectors.
OS Synchococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Tsinoremas N.F., Golden S.S.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44761; AAA86650.1; -.
SQ SEQUENCE 65 AA; 7546 MW; 0CF9C805E2E55EEB CRC64;

Query Match 100.0%; Score 20; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 17 DLDA 20

RESULT 15
Q50486 PRELIMINARY; PRT; 66 AA.
AC Q50486;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein SC05768.
GN SC05768 OR SC48.07C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Lark L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL020958; CAA15874.1; -.
KW Hypothetical protein.
SQ SEQUENCE 66 AA; 7391 MW; D962DA10258E6166 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 7 DLDA 10

RESULT 16
Q9L8X2 PRELIMINARY; PRT; 67 AA.
AC Q9L8X2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Polyketide synthase module 5 (Fragment).
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC15068;
RX MEDLINE=20179700; PubMed=10713461;
RA Xue Y., Wilson D., Sherman D.H.;
RT "Genetic architecture of the polyketide synthases for methymycin and
pikromycin series macrolides.";
RL Gene 245:203-211(2000).
DR EMBL; AF193251; AAF61859.1; -.
FT NON_TER 1
SQ SEQUENCE 67 AA; 6905 MW; 9A8A2E2F8EC1DF97 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 51 DLDA 54

RESULT 17
Q9L8X0 PRELIMINARY; PRT; 67 AA.
AC Q9L8X0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Polyketide synthase module 5 (Fragment).
OS Streptomyces narbonensis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 RN NCBI_TaxID=67333;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19790;
 RA MEDLINE=20179700; PubMed=107113461;
 RX Xue Y., Wilson D., Sherman D.H.;
 RT "Genetic architecture of the polyketide synthases for methymycin and
 RT pikromycin series macrolides.";
 RL Gene 245:203-211(2000).
 DR EMBL; AF193252; AAF61861.1; -.
 FT NON_TER
 SQ SEQUENCE 67 AA; 6841 MW; B7358A8954E4ED59 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 51 DLDA 54
 RESULT 18
 Q9KIL3
 ID Q9KIL3 PRELIMINARY; PRT; 69 AA.
 AC Q9KIL3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE F132r (Fragment).
 GN F132r.
 OS Streptomyces coelicolor A3(2).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=100226;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M145;
 RA Kormanec J., Sevcikova B., Homerova D.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF230493; AAF82067.1; -.
 FT NON_TER
 SQ SEQUENCE 69 AA; 7611 MW; F824D0F3BCECD7F9 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 58 DLDA 61
 RESULT 19
 Q9CIA6
 ID Q9CIA6 PRELIMINARY; PRT; 69 AA.
 AC Q9CIA6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Prophage pil protein 25.
 GN P125 OR LL0460.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;

RT The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006282; AAK04558.1; -.
 KW Complete proteome.
 SQ SEQUENCE 69 AA; 7893 MW; 2689487DF9E968E1 CRC64;
 Query Match 100.0%; Score 20; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 41 DLDA 44
 RESULT 20
 Q9TRL6
 ID Q9TRL6 PRELIMINARY; PRT; 70 AA.
 AC Q9TRL6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CORNEA-associated antigen, CO-AG-CALGRANULIN C homolog.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96181454; PubMed=8603881;
 RL Liu S.H., Gottsch J.D.;
 RT "Amino acid sequence of an immunogenic corneal stromal protein.";
 RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 DR HSSP; P80511; 1E8A.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS003407; CaBP_S100; 1.
 SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;
 Query Match 100.0%; Score 20; DB 6; Length 70;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLDA 4
 Db 59 DLDA 62
 RESULT 21
 Q9LD48
 ID Q9LD48 PRELIMINARY; PRT; 70 AA.
 AC Q9LD48;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE F14M2.2 protein (T3M13.13 protein).
 GN F14M2.2 OR T3M13.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Matti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC T3M13 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010164; AAF97294.1; -;
DR EMBL; AC022288; AAG52205.1; -;
SQ SEQUENCE 70 AA; 8139 MW; FC1B869C0C3534E0 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 25 DLDA 28

RESULT 22

Q92K57 ID Q92K57 PRELIMINARY; PRT; 70 AA.
AC Q92K57;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R02063.
GN R02063 OR SMC04324.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Kahn D., Kiss E., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46642.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 70 AA; 7140 MW; 6243942B93F1C99 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 46 DLDA 49

RESULT 23

O69718 ID O69718 PRELIMINARY; PRT; 71 AA.
AC O69718;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative integrase fragment.
GN RV3751 OR MTV025.099.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Stulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL; AL022121; CAA18073.1; -;
DR Tuberculist; RV3751; -;
DR InterPro; IPR002104; Phage_integrase.
DR Pfam; PF00589; Phage_integrase; 1.
KW Complete proteome.
SQ SEQUENCE 71 AA; 7584 MW; 4682AFA99F5D8145 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 55 DLDA 58

RESULT 24

Q92S57 ID Q92S57 PRELIMINARY; PRT; 72 AA.
AC Q92S57;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R00570.
GN R00570 OR SMC02266.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591784; CAC45142.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 72 AA; 7854 MW; 14D2ECF82376DC9 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 72;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 34 DLDA 37

RESULT 25

Q9YW97 ID Q9YW97 PRELIMINARY; PRT; 74 AA.
AC Q9YW97;

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Capsid protein homolog (Fragment).
OS Epiphyas postvittana nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=70600;
RN [1]
RN SEQUENCE FROM N.A.
RA Hyink O., Graves S., Fairbairn F.M., Ward V.K.;
RT "Mapping and Polyhedrin Gene Analysis of the Epiphyas postvittana
RL Nucleopolyhedrovirus Genome.";
RL J. Gen. Virol. 78:2853-2862(1998).
DR EMBL; AF061578; AAC72190.1; -
FT NON_TER 1
SQ SEQUENCE 74 AA; 8484 MW; 272B27213A310078 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 68 DLDA 71

RESULT 26
Q99YD3 PRELIMINARY; PRT; 74 AA.
AC Q99YD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acyl carrier protein (ACP).
OS ACPP OR SPV1753.
GN Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- FUNCTION: THIS PROTEIN IS THE CARRIER OF THE GROWING FATTY ACID
CC CHAIN IN FATTY ACID BIOSYNTHESIS (BY SIMILARITY).
DR EMBL; AE006603; AAK34496.1; -
DR HSSP; P02901; IACP.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Fatty acid biosynthesis; Phosphopantetheine; Complete proteome.
SQ SEQUENCE 74 AA; 8343 MW; 41D7F7F23065B44 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 27
Q9FBC6 PRELIMINARY; PRT; 74 AA.
AC Q9FBC6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Acyl carrier protein.
OS ACPP OR SP0418.
GN Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=R6;
RX MEDLINE=20365714; PubMed=10910344;
RA Heath R.J., Rock C.O.;
RT "A triclosan-resistant bacterial enzyme.";
RL Nature 406:145-146(2000).
RN [2]
RN SEQUENCE FROM N.A.
RA STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AF197933; AAF98272.1; -
DR EMBL; AE007353; AAK74581.1; -
DR HSSP; P02901; IACP.
DR TIGR; SP0418; -
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Phosphopantetheine; Complete proteome.
SQ SEQUENCE 74 AA; 8268 MW; E2E9A78567090C14 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 28
Q99QG6 PRELIMINARY; PRT; 74 AA.
AC Q99QG6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein SCP1.348.
GN SCP1.348 AND SCP1.06C.
OS Streptomyces coelicolor.
OG Plasmid SCP1.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=A3(2);
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

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RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL590464; CAC36873.1; -.
DR EMBL: AL590463; CAC36528.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 74 AA; 7940 MW; 48C43E8075052C08 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

RESULT 29
Q93EG1 PRELIMINARY; PRT; 75 AA.
AC Q93EG1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative citrate synthase (Fragment).
GN GLTA.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-3B1;
RA Ge Z., Feng Y., Fox J.G.;
RT "Helicobacter hepaticus genome: construction of an ordered cosmid
RT library and sequence analysis of the selected genomic regions.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF358704; AAL16694.1; -.
DR InterPro: IPR002020; Citrate_synth.
DR Pfam: PF00285; citrate_synth; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8591 MW; 4D2DD8290D6346B3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 17 DLDA 20

RESULT 30
P79246 PRELIMINARY; PRT; 75 AA.
AC P79246;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hormone-sensitive lipase (Fragment).
GN HSL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RX MEDLINE-96057569; PubMed-7549969;
RA Liu C.Y., Liang L.C., Chang L.C.;
RT "Differential responses of hormone-sensitive lipase gene to
RT nutritional transition in adipose tissue, liver, and skeletal muscle
RT of pigs.";
RL Biochem. Mol. Biol. Int. 36:689-694(1995).
RL EMBL: S80110; AAB47019.2; -.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8477 MW; 5B0B0684C98B4148 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 9 DLDA 12

RESULT 31
P93274 PRELIMINARY; PRT; 75 AA.
AC P93274;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Proline rich protein (Fragment).
GN PRP.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRANNY SMITH;
RA Dong Y.-H., Janssen B.J., Bielecki L.L., Atkinson R.G., Morris B.A.,
RA Gardner R.C.;
RT "Isolating and characterizing genes differentially expressed early in
RT apple fruit development.";
RL J. Am. Soc. Hortic. Sci. 122:752-757(1997).
DR EMBL: U80271; AAC06386.1; -.
DR HSSP; P24337; LHYP.
DR InterPro: IPR003612; AAI.
DR InterPro: IPR001768; Try/amyl_inhbtr.
DR Pfam: PF00234; tryp_alpha_amyl; 1.
DR SMART; SM00499; AAI; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 7643 MW; 694B833A59D8AD6F CRC64;

Query Match 100.0%; Score 20; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 31 DLDA 34

RESULT 32
Q85323 PRELIMINARY; PRT; 75 AA.
AC Q85323;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE D5R protein (Fragment).
GN D5R.
OS Vaccinia virus.

```

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IHD-W;
RX MEDLINE=94120724; PubMed=8291232;
RA Millon A.K., Carpenter M.S., DeLange A.M.;
RT "The vaccinia virus-encoded uracil DNA glycosylase has an essential
role in viral DNA replication.";
RL Virology 198:504-513(1994).
DR EMBL; L24385; AAA18016.2; -.
DR InterPro; IPR004968; Pox_D5.
DR Pfam; PF03288; Pox_D5; 1.
FT NON_TER 75
SQ SEQUENCE 75 AA; 8648 MW; 884EBCEB5B9560D8 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db | | | |
72 DLDA 75

RESULT 33
Q9Q8W0 PRELIMINARY; PRT; 76 AA.
AC Q9Q8W0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp118L.
GN S118L.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KASZA;
RX MEDLINE=84165064; PubMed=6323741;
RA Delange A.M., Macaulay C., Block W., Mueller T., McFadden G.;
RT "Tumorigenic poxviruses: construction of the composite physical map of
the Shope fibroma virus genome.";
RL J. Virol. 50:408-416(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KASZA;
RX MEDLINE=92074222; PubMed=1660196;
RA Strayer D.S., Jerng H.H., O'Connor K.;
RT "Sequence and analysis of a portion of the genomes of Shope fibroma
virus and malignant rabbit fibroma virus that is important for viral
replication in lymphocytes.";
RL Virology 185:585-595(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=KASZA;
RX MEDLINE=20032074; PubMed=10562495;
RA Willer D.O., McFadden G., Evans D.H.;
RT "The complete genome sequence of shope (Rabbit) fibroma virus.";
RL Virology 264:319-343(1999).
DR EMBL; AF170722; AAF18001.1; -.
SQ SEQUENCE 76 AA; 8549 MW; 7E636A24EBFAC0D7 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 76;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db | | | |
25 DLDA 28

RESULT 34

Q90Y04 PRELIMINARY; PRT; 76 AA.
AC Q90Y04;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ATP synthase alpha subunit (Fragment).
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
OC Estrilidae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RA Metzendorf R.;
RT "Effect of inhibition of aromatase on gene expression and behavior in
a songbird.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
DR EMBL; AF314256; AAL26859.1; -.
DR InterPro; IPR00793; ATPase_a/bc.
DR InterPro; IPR00790; ATPase_ac.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR ProDom; PD001099; ATPase_ac; 1.
KW ATP synthesis; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase.
FT NON_TER 1
FT NON_TER 76
SQ SEQUENCE 76 AA; 8431 MW; 83EFC5ADEB84970 CRC64;

Query Match 100.0%; Score 20; DB 13; Length 76;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db | | | |
2 DLDA 5

RESULT 35
O86536 PRELIMINARY; PRT; 76 AA.
AC O86536;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SCO5555.
GN SCO5555 OR SCIC2.36.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";

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RL Nature 417:141-147(2002).
DR EMBL; AL031124; CAA20003.1; -.
KW Hypothetical protein.
SQ SEQUENCE 76 AA; 8422 MW; 6AB2D84D0B80F560 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 65 DLDA 68

RESULT 36
Q9AN31 PRELIMINARY; PRT; 77 AA.
AC Q9AN31;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ID597.
GN ID597.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome."
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322013; AAG60947.1; -.
SQ SEQUENCE 77 AA; 8646 MW; 6205B1062AC86D00 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 46 DLDA 49

RESULT 37
Q9F774 PRELIMINARY; PRT; 77 AA.
AC Q9F774;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Acyl carrier protein (Acyl carrier protein, putative).
GN ACPP OR SP0038.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469436; PubMed=10903317;
RA McAllister K.A., Peery R.B., Meier T.I., Fischl A.S., Zhao G.;
RT "Biochemical and Molecular Analyses of the Streptococcus pneumoniae
RT Acyl Carrier Protein Synthase, an Enzyme Essential for Fatty Acid
RT Biosynthesis."
RL J. Biol. Chem. 275:30864-30872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
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RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae";
RL Science 293:498-506(2001).
DR EMBL; AF278618; AAG22707.1; -.
DR EMBL; AF007321; AAK74228.1; -.
DR TIGR; SP0038; -.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Phosphopantetheine; Complete proteome.
SQ SEQUENCE 77 AA; 8835 MW; 2CAB5EBE266AC256 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 33 DLDA 36

RESULT 38
Q92NC0 PRELIMINARY; PRT; 78 AA.
AC Q92NC0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein R02290.
GN R02290 OR SMC01546.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46869.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 78 AA; 8582 MW; 9B9ED1D2EA7A184E CRC64;

Query Match 100.0%; Score 20; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 24 DLDA 27

RESULT 39
Q9AZ98 PRELIMINARY; PRT; 79 AA.
AC Q9AZ98;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
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DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Orf79.
GN Lactobacillus johnsonii prophage Lj771.
OS Viruses.
OC NCBI_TaxID=139871;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=2045575; PubMed=10998330;
RX Desiere F., Fridmore R.D., Brussow H.;
RA "Comparative genomics of the late gene cluster from lactobacillus
RT phages.";
RL Virology 275:294-305(2000).
DR EMBL; AF195901; AAK27923.1;
SQ SEQUENCE 79 AA; 8717 MW; B2308AD37074A848 CRC64;

Query Match 100.0%; Score 20; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 32 DLDA 35

RESULT 40
O25449
ID O25449 PRELIMINARY; PRT; 79 AA.
AC O25449;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein HP0754.
GN HP0754.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000588; AAD07810.1;
DR TIGR; HP0754;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 79 AA; 9113 MW; DF076819852219BD CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 39 DLDA 42

RESULT 41
Q92L89
ID Q92L89 PRELIMINARY; PRT; 79 AA.
AC Q92L89
DT 01-MAY-1999 (TREMBlrel. 10, Created)

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DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PUTATIVE.
GN JHP0691.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.D., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001500; AAD06266.1;
KW Complete proteome.
SQ SEQUENCE 79 AA; 9059 MW; DF02C6102294A6FF CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 39 DLDA 42

RESULT 42
Q9A5F8
ID Q9A5F8 PRELIMINARY; PRT; 79 AA.
AC Q9A5F8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein CC2492.
GN CC2492.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005918; AAK24463.1;
DR TIGR; CC2492;
DR InterPro; IPR003850; UPF0062.
DR Pfam; PF02700; UPF0062;
DR TIGRFAMs; TIGR00302; TIGR00302;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 79 AA; 8551 MW; 2213A7E552E6F648 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 45 DLDA 48

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SQ SEQUENCE 79 AA; 9201 MW; C391948F6C51FD98 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
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|
|
DB 8 DLDA 11

RESULT 45

Q9LB27 PRELIMINARY; PRT; 80 AA.
AC Q9LB27;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-JUN-2001 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chitinase A (EC 3.2.1.14) (Fragment).
GN CHIA.
OS Chesapeake Bay isolate 6d.
OC Bacteria; Proteobacteria; gamma subdivision.
OX NCBI_TaxID=116867;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6D;
RX PubMed=11053737;
RA Ramaiah N., Hill R.T., Chun J., Ravel J., Matte M.H., Straube W.L.,
RA Colwell R.R.;
RT "Use of a chiA probe for detection of chitinase genes in bacteria from
the Chesapeake Bay.";
RL FEMS Microbiol. Ecol. 34:63-71(2000).
DR EMBL; AF059504; AAF37590.1;
DR HSSP; P07254; ICTN.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
KW Glycosidase; Hydrolase.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 8660 MW; 0F10CB9A71FAF84F CRC64;

Query Match 100.0%; Score 20; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
DB 39 DLDA 42

Search completed: February 6, 2003, 11:21:55
Job time : 24.3333 secs

RESULT 43

Q9A0C1 PRELIMINARY; PRT; 79 AA.
AC Q9A0C1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein SPY0841.
GN SPY0841.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Serate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Xuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006534; AAK33771.1;
DR InterPro; IPR004087; KH_dom.
DR Pfam; PF00013; KH-domain; 1.
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 79 AA; 8872 MW; 0B79DB869FBA433C CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
|
|
|
|
DB 38 DLDA 41

RESULT 44

Q926P1 PRELIMINARY; PRT; 79 AA.
AC Q926P1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein pli0011.
GN Pli0011.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Bloeker P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurupkat G.,
RA Madoeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
DR EMBL; AL592102; CAC42009.1;
KW Plasmid; Hypothetical protein; Complete proteome.

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 27.8333 Seconds
(without alignments)
19.150 Million cell updates/sec

Title: PAT943-3

Perfect score: 21

Sequence: 1 syda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 687

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*
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5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	5	23	AB06577
2	21	100.0	10	23	AB06548
3	21	100.0	12	20	AA032812
4	21	100.0	12	21	AA040040
5	21	100.0	13	21	AA039650
6	21	100.0	13	21	AA039682
7	21	100.0	22	17	AA05488
8	21	100.0	25	17	AA000324
9	21	100.0	36	14	AA040055
10	21	100.0	43	22	AA080858

11	21	100.0	43	23	AAU77652
12	21	100.0	50	20	AAW78216
13	21	100.0	51	22	AAE08853
14	21	100.0	51	23	AAU77647
15	21	100.0	56	22	AB017155
16	21	100.0	57	23	ABP33003
17	21	100.0	65	22	AB028160
18	21	100.0	65	22	AB028240
19	21	100.0	65	22	AB033335
20	21	100.0	65	22	AB033415
21	21	100.0	65	22	AB040153
22	21	100.0	65	22	AB018875
23	21	100.0	65	22	AB018874
24	21	100.0	65	22	AB024610
25	21	100.0	65	22	AB054200
26	21	100.0	65	22	AB060918
27	21	100.0	65	22	AA066514
28	21	100.0	65	22	AA066594
29	21	100.0	65	22	AA073603
30	21	100.0	65	22	AA014387
31	21	100.0	65	22	AA014467
32	21	100.0	65	22	AA020034
33	21	100.0	65	22	AA024454
34	21	100.0	65	22	AA026800
35	21	100.0	65	22	AA033798
36	21	100.0	65	22	AA021114
37	21	100.0	65	22	AA021194
38	21	100.0	65	22	AB036166
39	21	100.0	65	23	ABG36246
40	21	100.0	65	23	ABG43473
41	21	100.0	71	23	ABP05806
42	21	100.0	74	22	AB035040
43	21	100.0	74	22	AB035934
44	21	100.0	74	22	AB020450
45	21	100.0	74	22	AB020450

ALIGNMENTS

RESULT 1
AB06577
ID AB06577 standard; Peptide: 5 AA.
XX
AC AB06577;
XX
DT 31-MAY-2002 (first entry)
XX
DE Amyloid protein precursor mutagenic peptide SEQ ID NO:178.
XX
KW Beta-secretase: enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nontropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200206306-A2.
XX
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23035.
XX
PR 19-JUL-2000; 2000US-219795P.
PR 12-MAR-2001; 2001US-275251P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrichson RL;
XX
DR WPI; 2002-216995/27.
XX

C-terminus of chim
Human secreted pro
His-1c2 protein C-
C-terminus of chim
Human nervous syst
Human ORF1976 prot
Human peptide #811
Human peptide #891
Peptide #841 enco
Peptide #921 enco
Peptide #7659 enco
Protein #794 enco
Protein #873 enco
Protein #6609 enco
Human brain expres
Human brain expres
Human bone marrow
Human bone marrow
Peptide #821 enco
Peptide #901 enco
Peptide #6468 enco
Human EST encoded
Peptide #837 enco
Peptide #917 enco
Peptide #7835 enco
Peptide #796 enco
Peptide #876 enco
Human peptide enco
Human peptide enco
Human ORF1 protein
Peptide #2546 enco
Peptide #3440 enco
Protein #2449 enco

PT Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease

XX Example 8; Page 90; 188pp; English.

PS The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 21; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

Db 2 SYDA 5

RESULT 2

ABB06548
 ID ABB06548 standard; Peptide; 10 AA.

AC ABB06548;

XX 31-MAY-2002 (first entry)

DE Beta-secretase cleavage site peptide SEQ ID NO:143.

XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KW Alzheimer's disease.

OS Homo sapiens.

OS Synthetic.

XX WO200206306-A2.

XX 24-JAN-2002.

XX 19-JUL-2001; 2001WO-US23035.

XX 19-JUL-2000; 2000US-219795P.

XX 12-MAR-2001; 2001US-275251P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrichson RL;

XX WPI; 2002-216995/27.

XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease

XX Claim 20; Page 169; 188pp; English.

XX The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate

CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 21; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

Db 4 SYDA 7

RESULT 3

AAV32812
 ID AAV32812 standard; peptide; 12 AA.

XX AAV32812;

XX 09-NOV-1999 (first entry)

XX Vascular endothelial growth factor receptor 3 polypeptide.

XX Signal transduction; proteolytic cleavage; renal tubular defect; uraemia;
 KW proteosome binding site; muscle wasting; eating disorder; AIDS;
 KW diabetes; Cushing's disease; growth hormone deficiency; inhibitor;
 KW ubiquitin; vascular endothelial growth factor receptor 3.

OS Synthetic.

XX EP943624-A1.

XX 22-SEP-1999.

XX 12-MAR-1998; 98EP-0200799.

XX 12-MAR-1998; 98EP-0200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

XX Controlling the availability and/or signal transduction capability
 PT of a cell surface receptor, useful for treating growth hormone
 PT deficiencies

XX Disclosure; Page 10; 36pp; English.

XX This sequence is a polypeptide from the vascular endothelial growth
 CC factor receptor 3. Sequences (AAV32794-Y32823) are examples of
 CC polypeptide sequences found at or near the ubiquitin/proteosome complex
 CC binding site located on the intracellular part of a cell surface
 CC receptor. These sequences are used in a method for controlling the
 CC availability and signal transduction capability of a cell surface
 CC receptor by administering an inhibitor that is capable of inhibiting
 CC proteolytic cleavage of the receptor. Inhibition of this proteolytic
 CC cleavage results in the receptors being present on the surface for longer
 CC and therefore signalling for longer to any hormones which might be
 CC increases the sensitivity of cells to any hormones which might be
 CC present. The inhibitor is either derived from, competes with or binds to
 CC a polypeptide sequence of which sequences AAV32794-Y32823 are examples.
 CC The inhibitor may be used to treat muscle wasting, associated with

CC disorders such as renal tubular defects, uraemia, diabetes, Cushing's
 CC syndrome, cachexias, eating disorders, AIDS, after stress and during
 CC neuromuscular disease.

XX Sequence 12 AA;

Query Match 100.0%; Score 21; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
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 Db 9 SYDA 12

RESULT 4

AAB40040
 ID AAB40040 standard; Peptide; 12 AA.

XX AAB40040;

XX 05-FEB-2001 (first entry)

XX Anti-hIL12 antibody light chain CDR3 amino acid sequence SEQ ID 556.

XX Human; neutralising antibody; Interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI) BASF AG.

XX (GEMY) GENETICS INST INC.

XX Salfeld JG, Roques M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

XX Claim 32; Figure 2H; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC51062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment

CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 12 AA;

Query Match 100.0%; Score 21; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 2 SYDA 5

RESULT 5

AAB39650

ID AAB39650 standard; Peptide; 13 AA.

XX AAB39650;

XX 05-FEB-2001 (first entry)

XX Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 166.

XX Human; neutralising antibody; Interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI) BASF AG.

XX (GEMY) GENETICS INST INC.

XX Salfeld JG, Roques M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

XX Example 1; Page 127; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.

CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 SQ

Sequence 13 AA;

Query Match 100.0%; Score 21; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
 ||||
 Db 2 SYDA 5

RESULT 6

AAW05488
 ID AAW05488 standard; Peptide; 13 AA.

XX AAW05488;

AC AAW05488;

XX 05-FEB-2001 (first entry)

DT Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 198.
 DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritis;
 KW antisclerotic; neuroprotective; antiprosclerotic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

OS WO2000056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI) BASF AG.

XX (GEMY) GENETICS INST INC.

XX Sajfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaynakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warner NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to

PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 PT

PS Example 1; Page 128; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritis; antisclerotic;
 CC antiinflammatory; neuroprotective; antiprosclerotic; antiasthmatic;

CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 SQ

Sequence 13 AA;

Query Match 100.0%; Score 21; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
 ||||
 Db 2 SYDA 5

RESULT 7

AAW05488

ID AAW05488 standard; Peptide; 22 AA.

XX AAW05488;

AC AAW05488;

XX 24-FEB-1998 (first entry)

DE SH3-binding peptide P53PB2.P5.
 XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
 KW cellular signalling element; cellular structural element; malignancy;
 KW protein identification; functional domain; protein screening;
 KW cellular signal transduction process; binding peptide.

XX Synthetic.

XX WO9631625-A1.

XX 10-OCT-1996.

XX 04-APR-1996; 96WO-US04454.

XX 03-APR-1996; 96US-0630915.

XX 07-APR-1995; 95US-0417872.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;

XX WPI; 1996-465045/46.

XX Identifying polypeptide(s) having specific functional domain (esp.
 SH3 domain) - comprises detecting selective binding to recognition
 unit, regardless of sequence homology

XX Example; Fig 13; 174pp; English.

XX AAW05445-WO5492 represent Src-homology region 3 (SH2) domain binding
 CC peptides. These sequences were used as parts of multivalent recognition
 CC unit complexes used in the method of the invention. The method of the
 CC invention is for identifying polypeptides containing functional domains
 CC of interest (especially SH3 domains). It comprises contacting a
 CC multivalent recognition unit (RU) complex with a number of peptides and
 CC identifying polypeptides having a selective binding affinity for the RU
 CC complex. The method is based on functional similarities and does not
 CC rely on sequence similarities. Prior methods only gave limited success
 CC for identifying proteins containing an SH3 domain due to the minimal
 CC sequence homology among known SH3 proteins. Multivalent RU complexes are
 CC particularly suited to screening for polypeptides containing functional
 CC domains that are similar to, but not identical in sequence to, the
 CC original target functional domain. The new method enables proteins
 CC having a common function to be identified. Identification of novel SH3
 CC proteins will be useful for a better understanding of cell growth,

CC malignancy, signal transduction processes, etc. New candidate drugs can
 CC be identified, and their specificities (e.g. pharmacological activities)
 CC can be assessed using the method of the invention.

XX Sequence 22 AA;

Query Match 100.0%; Score 21; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 1 SYDA 4

RESULT 8

AAW00324
 ID AAW00324 standard; peptide; 25 AA.

XX AC
 XX AAW00324;

XX DT 23-JUN-1997 (first entry)

XX DE Human I-kappa-B-alpha residues 279-303, variant Thr291Ala.

XX KW Human; I-kappa-B-alpha; transcription factor; inhibitor; variant;
 KW inhibition; suppression; phosphorylation; antiinflammation;
 KW immunosuppression; antiinflammatory; immunosuppressant; mutant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 13 /note= "wild type Thr substituted with Ala"

XX PN W09632412-Al.

XX PD 17-OCT-1996.

XX PF 12-APR-1996; 96WO-JP01028.

XX PR 13-APR-1995; 95JP-0111033.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PA (CHUS) CHUGAI PHARM CO LTD.

XX PI Ishikawa Y, Kuno K, Matsushima K;

XX DR WPI; 1996-477071/47.

XX PT Peptide(s) which suppress the phosphorylation of I-kappa-B-alpha -
 PT act as effective antiinflammatory and immunosuppressant agents

XX PS Example 1; Page 29; 43pp; Japanese.

XX CC The present peptide, which comprises residues 279-303 of human
 CC I-kappa-B-alpha (a transcription factor inhibitor) and the mutation
 CC Thr291Ala, suppresses I-kappa-B-alpha phosphorylation. It can be
 CC used as an antiinflammatory or immunosuppressant, at a preferred
 CC dosage of 0.001-1000 (particularly 0.01-10) mg/day orally or
 CC non-orally.

XX SQ Sequence 25 AA;

Query Match 100.0%; Score 21; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 10 SYDA 13

RESULT 9
 AAR40055

XX ID AAR40055 standard; peptide; 36 AA.

XX AC AAR40055;

XX DT 04-FEB-1994 (first entry)

XX DE Hib OMP P1 peptide HIBP1-3 (103-137).

XX KW Haemophilus influenzae; type b; Hib; outer membrane protein; P1; P2;
 KW P6; vaccine; antibody; detection; lipoglycopeptide conjugate;
 KW immunogen.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1 /note= "May be absent"

XX PN W09315205-A.

XX PD 05-AUG-1993.

XX PF 03-FEB-1993; 93WO-CA00041.

XX PR 03-FEB-1992; 92GB-0002219.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Chong P, Kandil A, Klein MH, Sia C;

XX DR WPI; 1993-258681/32.

XX PT Synthetic Haemophilus influenzae conjugate vaccine - comprising
 PT T-helper cell determinants and B-cell epitope(s) linked to
 PT synthetic oligo:saccharide(s)

XX PS Table 1; Page 47; 99pp; English.

XX CC The sequences given in AAR40053-101 are peptide fragments derived from
 CC the Haemophilus influenzae type b (Hib) outer membrane proteins P1,
 CC P2 and P6. These peptides may be used in a vaccine against Hib
 CC infection and antibodies against these peptides may be used in test
 CC kits to detect H. influenzae in a sample. The vaccine may further
 CC comprise an immunogenic or immunostimulatory molecule or the peptides
 CC may be modified with lipids, or linked to synthetic PRP as synthetic
 CC lipoglycopeptide conjugates to produce alternative vaccines.

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 21; DB 14; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 25 SYDA 28

RESULT 10

AAE08858

XX ID AAE08858 standard; peptide; 43 AA.

XX AC AAE08858;

XX DT 15-NOV-2001 (first entry)

XX DE Escherichia coli chimeric CspA protein C-terminal peptide 1c2.

XX KW Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;
 KW washing powder; cold shock protein; CspA.

```

OS Chimeric - Escherichia coli.
XX Chimeric - Unidentified.
XX WO200157065-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-GB00445.
XX
XX 03-FEB-2000; 2000GB-0002492.
XX
XX 04-FEB-2000; 2000US-0180326.
XX
XX 03-JUL-2000; 2000GB-0016346.
XX
XX 07-AUG-2000; 2000GB-0019362.
XX
XX (DIVE-) DIVERSYS LTD.
XX
XX Riechmann L, Winter G;
XX
XX WPI; 2001-529779/58.
XX
XX Chimeric folded protein domain derived from repertoire of chimeric
XX proteins useful therapeutically, comprises two or more sequence
XX segments derived from parent amino acid sequence that are
XX non-homologous -
XX
XX Example 16; Page 47; 75pp; English.
XX
XX The invention relates to a chimeric folded protein domain derived from
XX a repertoire of chimeric proteins. The chimeric protein comprises two or
XX more sequence segments derived from parent amino acid sequence that are
XX non-homologous. The chimeric protein is useful in vaccination against
XX one or more of the amino acid sequences from which the chimera is
XX derived, for administration to a human for therapeutic purposes, and for
XX use in a commercial product to which humans are exposed. The chimeric
XX protein is useful as improved enzyme inhibitors, and to avoid
XX sensitisation in humans (for e.g. enzymes and washing powders). The
XX present sequence is Escherichia coli cold shock protein (CspA)
XX C-terminal peptide chimeric protein used in the exemplification of
XX the invention.
XX
XX Sequence 43 AA;
XX
XX Query Match 100.0%; Score 21; DB 22; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SYDA 4
XX ||||
XX Db 17 SYDA 20
XX
XX RESULT 11
XX AAU77652
XX ID AAU77652 standard; Peptide; 43 AA.
XX
XX AC AAU77652;
XX
XX XX
XX 05-JUN-2002 (first entry)
XX
XX DE C-terminus of chimaeric protein 1c2.
XX
XX RhsD; chimaeric folded protein domain; 1c2; vaccine; asthma;
XX proteolysis resistance.
XX
XX KW Escherichia coli.
XX
XX OS Synthetic.
XX
XX PN WO200212277-A2.
XX
XX XX
XX 14-FEB-2002.
XX
XX PF 03-AUG-2001; 2001WO-GB03508.
XX

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PR 07-AUG-2000; 2000GB-0019362.
PR 02-FEB-2001; 2001GB-0002678.
XX
XX (DIVE-) DIVERSYS LTD.
XX
XX Riechmann L, Winter G;
XX
XX WPI; 2002-257461/30.
XX
XX Novel chimaeric folded protein domain, useful in vaccination, is derived
XX from a repertoire of chimaeric proteins and comprises two or more
XX sequence segments derived from parent non-homologous sequences -
XX
XX Example 6; Page 61; 94pp; English.
XX
XX The invention relates to a chimaeric folded protein domain, when derived
XX from a repertoire of chimaeric proteins comprises two or more sequence
XX segments derived from parent amino acid sequences that are non-
XX homologous. Also included are nucleic acids encoding the chimaeric
XX protein domains and a method of producing the protein domains.
XX Chimaeric proteins His-2f3 and His-1c2 were used for immunisation of a
XX rabbit to analyse, if resulting antisera from the immunised animals are
XX crossreactive with CspA. The animals were then challenged with an
XX injection of folded cold shock protein (CspA) to see if a specific
XX anti-CspA immune response involving T cell mediated help was
XX established during immunisation. The analyses of the rabbit immune
XX response showed, that immunisation with both 2f3 and 1c2 raised
XX antisera highly reactive with their respective antigen as they bound
XX phage displaying the chimaeric proteins strongly after the second, third
XX and fourth vaccination. Crossreactivity with CspA was observed.
XX The protein domain is useful in vaccination against parent proteins from
XX which the chimera is derived, for administration to a human for
XX therapeutic purposes and for use in commercial product to which humans
XX are exposed. The protein domains are useful for treating asthma and in
XX immunisation. The chimaeric folded protein domain is resistant to in vivo
XX or in vitro proteolysis by protease enzymes and is not immunogenic or
XX weakly immunogenic, and hence suitable for therapeutic purposes and to
XX avoid sensitisation in humans. The present sequence is the C-terminus of
XX a chimaeric folded protein domain of the invention based on E.coli RhsD.
XX
XX Sequence 43 AA;
XX
XX Query Match 100.0%; Score 21; DB 23; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SYDA 4
XX ||||
XX Db 17 SYDA 20
XX
XX RESULT 12
XX AAW78216
XX ID AAW78216 standard; Protein; 50 AA.
XX
XX AC AAW78216;
XX
XX XX
XX 13-APR-1999 (first entry)
XX
XX DE Human secreted protein encoded by gene 34 clone HTTCN24.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX OS Homo sapiens.
XX
XX XX
XX Key Location/Qualifiers
XX

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FT Misc-difference 50
 XX /label= unknown

PN W09856804-A1.

XX 17-DEC-1998.

XX 11-JUN-1998; 98WO-US12125.

XX 02-OCT-1997; 97US-0061060.

XX 13-JUN-1997; 97US-0049547.

XX 13-JUN-1997; 97US-0049548.

XX 13-JUN-1997; 97US-0049549.

XX 13-JUN-1997; 97US-0049550.

XX 13-JUN-1997; 97US-0049606.

XX 13-JUN-1997; 97US-0049607.

XX 13-JUN-1997; 97US-0049608.

XX 13-JUN-1997; 97US-0049609.

XX 13-JUN-1997; 97US-0049610.

XX 13-JUN-1997; 97US-0049611.

XX 13-JUN-1997; 97US-0050566.

XX 13-JUN-1997; 97US-0050901.

XX 13-JUN-1997; 97US-0052989.

XX 08-JUL-1997; 97US-0051919.

XX 18-AUG-1997; 97US-0055984.

XX 12-SEP-1997; 97US-0058665.

XX 12-SEP-1997; 97US-0058668.

XX 12-SEP-1997; 97US-0058669.

XX 12-SEP-1997; 97US-0058750.

XX 12-SEP-1997; 97US-0058971.

XX 12-SEP-1997; 97US-0058972.

XX 12-SEP-1997; 97US-0058975.

XX 02-OCT-1997; 97US-0060834.

XX 02-OCT-1997; 97US-0060841.

XX 02-OCT-1997; 97US-0060844.

XX 02-OCT-1997; 97US-0060865.

XX 02-OCT-1997; 97US-0061059.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;

XX Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;

XX Yu GL;

XX WPI; 1999-080881/07.

XX N-PSDB; AAX04401.

XX New isolated human genes and the secreted polypeptides they encode -

FT useful for diagnosis and treatment of e.g. cancers, neurological

XX disorders, immune diseases, inflammation or blood disorders

XX Claim 11; Page 314; 380pp; English.

XX This sequence represents a secreted human protein encoded by the gene

XX clone detailed in the descriptor line. The gene can be used to generate

XX fusion proteins by linking to the gene to a human immunoglobulin Fc

XX portion (e.g. AAX04302) for increasing the stability of the fused

XX protein as compared to the human protein only.

XX The invention relates to 86 novel genes and their fragments (nucleic

XX acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)

XX which are useful for preventing, treating or ameliorating medical

XX conditions e.g. by protein or gene therapy. Also, pathological

XX conditions can be diagnosed by determining the amount of the new

XX polypeptides in a sample or by determining the presence of mutations in

XX the new polynucleotides. Specific uses are described for each of the 86

XX polynucleotides, based on which tissues they are most highly expressed in

XX (see AAX04311 for described uses).

XX Sequence 50 AA;

XX Query Match 100.0%; Score 21; DB 20; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SYDA 4

Db 22 SYDA 25

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RESULT 13

AAE08853

ID AAE08853 standard; peptide; 51 AA.

XX AAE08853;

XX 15-NOV-2001 (first entry)

XX His-1c2 protein C-terminal peptide sequence.

XX Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;

XX washing powder; His-1c2.

XX Unidentified.

XX WO200157065-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-GB00445.

XX 03-FEB-2000; 2000GB-0002492.

XX 04-FEB-2000; 2000US-0180326.

XX 03-JUL-2000; 2000GB-0016346.

XX 07-AUG-2000; 2000GB-0019362.

XX (DIVE-) DIVERSYS LTD.

XX Riechmann L, Winter G;

XX WPI; 2001-529779/58.

XX Chimeric folded protein domain derived from repertoire of chimeric

XX proteins useful therapeutically, comprises two or more sequence

XX segments derived from parent amino acid sequence that are

XX non-homologous -

XX Example 16; Page 46; 75pp; English.

XX The invention relates to a chimeric folded protein domain derived from

XX a repertoire of chimeric proteins. The chimeric protein comprises two or

XX more sequence segments derived from parent amino acid sequence that are

XX non-homologous. The chimeric protein is useful in vaccination against

XX one or more of the amino acid sequences from which the chimera is

XX derived, for administration to a human for therapeutic purposes, and for

XX use in a commercial product to which humans are exposed. The chimeric

XX protein is useful as improved enzyme inhibitors, and to avoid

XX sensitisation in humans (for e.g. enzymes and washing powders). The

XX present sequence is C-terminal peptide sequence of His-1c2 protein used

XX in the exemplification of the invention.

XX Sequence 51 AA;

Query Match 100.0%; Score 21; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4

Db 20 SYDA 23

1111

RESULT 14

AAU77647

ID AAU77647 standard; Peptide; 51 AA.

XX AAU77647;

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XX 05-JUN-2002 (first entry)
 XX C-terminus of chimaeric protein His-lc2.
 XX CspA; chimaeric folded protein domain; His-lc2;
 KW cold shock protein; vaccine; asthma; proteolysis resistance.
 XX Escherichia coli.
 OS Synthetic.
 XX WO200212277-A2.
 XX 14-FEB-2002.
 XX 03-AUG-2001; 2001WO-GB03508.
 XX 07-AUG-2000; 2000GB-0019362.
 PR 02-FEB-2001; 2001GB-0002678.
 XX (DIVE-) DIVERSYS LTD.
 XX Riechmann L, Winter G;
 XX WPI; 2002-257461/30.
 XX Novel chimaeric folded protein domain, useful in vaccination, is derived
 PT from a repertoire of chimaeric proteins and comprises two or more
 PT sequence segments derived from parent non-homologous sequences -
 XX Example 4; Page 60; 94pp; English.
 XX The invention relates to a chimaeric folded protein domain, when derived
 CC from a repertoire of chimaeric proteins comprises two or more sequence
 CC segments derived from parent amino acid sequences that are non-
 CC homologous. Also included are nucleic acids encoding the chimaeric
 CC protein domains and a method of producing the protein domains.
 CC Chimaeric proteins His-2f3 and His-lc2 were used for immunisation of a
 CC rabbit to analyse, if resulting antisera from the immunised animals are
 CC crossreactive with CspA. The animals were then challenged with an
 CC injection of folded cold shock protein (CspA) to see if a specific
 CC anti-CspA immune response involving T cell mediated help was
 CC established during immunisation. The analyses of the rabbit immune
 CC response showed, that immunisation with both 2f3 and lc2 raised
 CC antisera highly reactive with their respective antigen as they bound
 CC phage displaying the chimaeric proteins strongly after the second, third
 CC and fourth vaccination. Crossreactivity with CspA was observed.
 CC The protein domain is useful in vaccination against parent proteins from
 CC which the chimaera is derived, for administration to a human for
 CC therapeutic purposes and for use in commercial product to which humans
 CC are exposed. The protein domains are useful for treating asthma and in
 CC immunisation. The chimaeric folded protein domain is resistant to in vivo
 CC or in vitro proteolysis by protease enzymes and is not immunogenic or
 CC weakly immunogenic, and hence suitable for therapeutic purposes and to
 CC avoid sensitisation in humans. The present sequence is the C-terminus of
 CC a chimaeric folded protein domain, of the invention based on E.coli CspA.
 XX Sequence 51 AA;
 SQ Query Match 100.0%; Score 21; DB 23; Length 51;
 Best Local Similarity 100.0%; Preq. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDA 4
 Db 20 SYDA 23
 RESULT 15
 ID ABB17155 standard; Protein; 56 AA.
 XX ABB17155;
 AC ABB17155;

XX 23-JAN-2002 (first entry)
 XX Human nervous system related polypeptide SEQ ID NO 5812.
 XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX Homo sapiens.
 XX WO200159063-A2.
 XX 16-AUG-2001.
 XX 17-JAN-2001; 2001WO-US01334.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0218880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.

KW hypothyroidism; cholesterol ester storage disease; infection; vulneryary;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antihypertoid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.
XX Homo sapiens.
XX WO200190366-A2.
XX 29-NOV-2001.
XX 24-MAY-2001; 2001WO-US17076.
PF 24-MAY-2000; 2000US-206690P.
XX (CURA-) CURAGEN CORP.
XX Leach MD, Shinkets RA;
PI WPI; 2002-106200/14.
DR N-PSDB; ABN77029.
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
transplantation -
XX Claim 10; Page 1246; 2508pp; English.
XX Sequences ABP31028-ABP3561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN7587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases.
XX SQ Sequence 57 AA;

Query Match 100.0%; Score 21; DB 23; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYDA 4
|||||

Db 8 SYDA 11
RESULT 17
ABB28160
ID ABB28160 standard; Peptide; 65 AA.
XX ABB28160;
AC ABB28160;
DT 01-FEB-2002 (first entry)
XX Human peptide #811 encoded by breast cell single exon nucleic acid probe.
DE Human; microarray; single exon probe; gene expression; breast;
XX Human; cancer.
KW Homo sapiens.
XX WO200157271-A2.
PN 09-AUG-2001.
PD 30-JAN-2001; 2001WO-US00662.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX Claim 27; SEQ ID NO 11128; 327pp + sequence listing; English.
PS The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYDA 4
|||||
Db 28 SYDA 31

RESULT 18
ABB28240
ID ABB28240 standard; Peptide; 65 AA.
XX
AC ABB28240;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human peptide #891 encoded by breast cell single exon nucleic acid probe.
XX
DE Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX
PS Claim 27; SEQ ID NO 11208; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
|||||
DB 36 SYDA 39

RESULT 19
ABB33335
ID ABB33335 standard; Peptide; 65 AA.
XX
AC ABB33335;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #841 encoded by human foetal liver single exon probe.
XX
DE Human; foetal liver; gene expression; single exon nucleic acid probe.
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX
PS Claim 27; SEQ ID NO 25970; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
|||||
DB 28 SYDA 31

RESULT 20
ABB33415
ID ABB33415 standard; Peptide; 65 AA.
XX
AC ABB33415;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #921 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX

OS Homo sapiens.
PN WO200157277-A2.
XX
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 27; SEQ ID NO 26050; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 AA;
SQ
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 36 SYDA 39
RESULT 21
ABB40153
ID ABB40153 standard; Peptide; 65 AA.
XX
XX ABB40153;
AC
XX
XX 04-FEB-2000 (first entry)
DT
XX
DE Peptide #7659 encoded by human foetal liver single exon probe.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00669.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 27; SEQ ID NO 32788; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 AA;
SQ
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 22 SYDA 25
RESULT 22
ABB18795
ID ABB18795 standard; Protein; 65 AA.
XX
XX ABB18795;
AC
XX
XX 23-JAN-2002 (first entry)
DT
XX
DE Protein #794 encoded by probe for measuring heart cell gene expression.
XX
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00666.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
PT

XX Claim 15; SEQ ID No 20565; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart (see

XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

XX probe. The probes may be used for predicting, measuring and displaying

XX gene expression in samples derived from the human heart via microarrays.

XX By measuring gene expression, the probes are useful for predicting,

XX diagnosing, grading, staging, monitoring and prognosing diseases of the

XX human heart and vascular system e.g. cardiovascular disease,

XX hypertension, cardiac arrhythmias and congenital heart disease.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4

DB 28 SYDA 31

RESULT 23

ID ABB18874 standard; Protein; 65 AA.

XX ABB18874;

XX 23-JAN-2002 (first entry)

DE Protein #873 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

XX Homo sapiens.

OS WO200157274-A2.

PN 09-AUG-2001.

PR 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488899/53.

DR Single exon nucleic acid probes for analyzing gene expression in human

XX hearts -

PS Claim 15; SEQ ID No 20644; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart (see

XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

XX probe. The probes may be used for predicting, measuring and displaying

XX gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosing diseases of the

CC human heart and vascular system e.g. cardiovascular disease,

CC hypertension, cardiac arrhythmias and congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4

DB 36 SYDA 39

RESULT 24

ID ABB24610 standard; Protein; 65 AA.

XX ABB24610;

XX 23-JAN-2002 (first entry)

DE Protein #609 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

XX Homo sapiens.

OS WO200157274-A2.

PN 09-AUG-2001.

PR 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488899/53.

DR Single exon nucleic acid probes for analyzing gene expression in human

XX hearts -

PS Claim 15; SEQ ID No 26380; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart (see

XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

XX probe. The probes may be used for predicting, measuring and displaying

XX gene expression in samples derived from the human heart via microarrays.

XX By measuring gene expression, the probes are useful for predicting,

XX diagnosing, grading, staging, monitoring and prognosing diseases of the

XX human heart and vascular system e.g. cardiovascular disease,

XX hypertension, cardiac arrhythmias and congenital heart disease.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

```
SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 25
AAM54200
ID AAM54200 standard; Protein; 65 AA.
XX AC
XX AC AAM54200;
XX AC
XX AC
DT 05-NOV-2001 (first entry)
XX DE
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26305.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer.
XX OS Homo sapiens.
XX OS
XX PN WO200157275-A2.
XX PN
XX PD 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US00667.
XX PF
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI
XX DR WPI; 2001-483446/52.
XX DR
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains -
XX PS Example 4; SEQ ID NO: 26305; 650pp + Sequence Listing; English.
XX PS
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention.
XX CC
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 36 SYDA 39

RESULT 26
AAM60918
ID AAM60918 standard; Protein; 65 AA.
XX AC
XX AC AAM60918;
XX AC
XX AC
DT 05-NOV-2001 (first entry)
XX DE
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33023.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer.
XX OS Homo sapiens.
XX OS
XX PN WO200157275-A2.
XX PN
XX PD 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US00667.
XX PF
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PR
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI
XX DR WPI; 2001-483446/52.
XX DR
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains -
XX PS Example 4; SEQ ID NO: 26305; 650pp + Sequence Listing; English.
XX PS
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention.
XX CC
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 36 SYDA 39

RESULT 27
AAM66514
ID AAM66514 standard; Protein; 65 AA.
XX AC
XX AC AAM66514;
XX AC
XX AC
DT 06-NOV-2001 (first entry)
XX DE
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26820.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX OS
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PN WO200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 26820; 658pp + Sequence Listing; English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX Sequence 65 AA;
 XX Query Match 100.0%; Score 21; DB 22; Length 65;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDA 4
 DB 28 SYDA 31
 RESULT 28
 AAM66594
 ID AAM66594 standard; Protein; 65 AA.
 AC AAM66594;
 XX 06-NOV-2001 (first entry)
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26900.
 DE Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 KW Homo sapiens.
 OS WO200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 26900; 658pp + Sequence Listing; English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 26900; 658pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX Sequence 65 AA;
 XX Query Match 100.0%; Score 21; DB 22; Length 65;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYDA 4
 DB 36 SYDA 39
 RESULT 29
 AAM73603
 ID AAM73603 standard; Protein; 65 AA.
 AC AAM73603;
 XX 06-NOV-2001 (first entry)
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 33909.
 DE Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 KW Homo sapiens.
 OS WO200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 33909; 658pp + Sequence Listing; English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a

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CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 30
AAM14387
ID AAM14387 standard; Protein; 65 AA.
XX
AC AAM14387;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #821 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 19213; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||

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Db 28 SYDA 31

RESULT 31
AAM14467
ID AAM14467 standard; Protein; 65 AA.
XX
AC AAM14467;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #901 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 19293; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||
Db 36 SYDA 39

RESULT 32
AAM20034
ID AAM20034 standard; Protein; 65 AA.
XX
AC AAM20034;
XX
DT 12-OCT-2001 (first entry)

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XX DE Peptide #6468 encoded by probe for measuring cervical gene expression.
XX KW Probe: human; microarray; gene expression; cervical epithelial cell;
KW KW cervical cancer.
XX OS Homo sapiens.
XX XX WO200157278-A2.
XX PN 09-AUG-2001.
XX PD 30-JAN-2001; 2001WO-US00670.
XX PF 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488901/53.
XX DR Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human cervical epithelial cells -
XX PS Claim 27; SEQ ID No 24860; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 22 SYDA 25
RESULT 33
AAM24454
ID AAM24454 standard; Protein; 65 AA.
XX AC AAM24454;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST encoded protein SEQ ID NO: 1979.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW KW diagnostics; forensic test; gene mapping; genetic disorder;
KW KW biodiversity; gene therapy; nutrition.
XX OS Homo sapiens.
XX XX

PN WO200154477-A2.
XX 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX XX WPI; 2001-476164/51.
XX DR N-PSDB; AAH99113.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use -
XX PS Claim 20; Page 1258-1259; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a
XX CC protein of the invention.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 37 SYDA 40
RESULT 34
AAM26800
ID AAM26800 standard; Protein; 65 AA.
XX AC AAM26800;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #837 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX XX WO200157272-A2.
XX PN 09-AUG-2001.
XX PD 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 27; SEQ ID No 27069; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 28 SYDA 31
|||||
RESULT 35
AAM26880
ID AAM26880 standard; Protein; 65 AA.
XX AC AAM26880;
XX 17-OCT-2001 (first entry)
XX Peptide #917 encoded by probe for measuring placental gene expression.
DE Peptide #917 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00663.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 27; SEQ ID No 27149; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 36 SYDA 39
|||||
RESULT 36
AAM33798
ID AAM33798 standard; Protein; 65 AA.
XX AC AAM33798;
XX 17-OCT-2001 (first entry)
XX Peptide #7835 encoded by probe for measuring placental gene expression.
DE Peptide #7835 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00663.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 27; SEQ ID No 34067; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
Db 22 SYDA 25
|||||
RESULT 37

KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.

OS Homo sapiens.

PN WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.

XX 04-FEB-2000; 2000US-180312P.

PR 26-MAY-2000; 2000US-207456P.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -

XX Claim 27; SEQ ID No 25831; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene
XX expression analysis, and for identifying exons in a gene, particularly
XX using human lung derived mRNA and for the study of lung diseases
XX such as asthma, lung cancer, chronic obstructive pulmonary disease
XX (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
XX fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
XX Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
XX haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
XX pulmonary alveolar proteinosis, Karagenen syndrome, fibrocystic
XX pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
XX and hyaline membrane disease. The present sequence is a peptide/protein
XX encoded by a single exon probe of the invention.

XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;
Best Local Similarity 100.0%; Pred. NO. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
Db 28 SYDA 31

RESULT 40

ABG36246

ID ABG36246 standard; Peptide; 65 AA.

XX AC ABG36246;

XX DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 25911.

XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US00665.

XX PR 04-FEB-2000; 2000US-180312P.

PR 26-MAY-2000; 2000US-207456P.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -

XX Claim 27; SEQ ID No 25911; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,

comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 36 SYDA 39

RESULT 41

ABG43473
 ID ABG43473 standard; Peptide; 65 AA.

AC ABG43473;

XX 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 33138.

KW Human: single exon probe: asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

OS Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.

XX 04-FEB-2000; 2000US-180312P.

XX 26-MAY-2000; 2000US-207456P.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -

XX Claim 27; SEQ ID No 33138; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
 ||||
 Db 22 SYDA 25

RESULT 42

ABP05806

ID ABP05806 standard; Protein; 71 AA.

XX ABP05806;

XX 24-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:11594.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US10836.
XX
XX 30-MAY-2000; 2000US-206132P.
PR 29-AUG-2000; 2000US-228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach MD;
XX
XX WPI: 2002-106308/14.
DR N-PSDB; ABN21558.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -
XX
XX Disclosure; SEQ ID 11594; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 71 AA;
SQ
Query Match 100.0%; Score 21; DB 23; Length 71;
Best Local Similarity 100.0%; Pred. NO. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
DB 6 SYDA 9
RESULT 43
ABB35040
ID ABB35040 standard; Peptide; 74 AA.
XX
AC ABB35040;
XX

XX 04-FEB-2002 (first entry)
DT Peptide #2546 encoded by human foetal liver single exon probe.
DE Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI: 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
PT
XX Claim 27; SEQ ID NO 27675; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 74 AA;
SQ
Query Match 100.0%; Score 21; DB 22; Length 74;
Best Local Similarity 100.0%; Pred. NO. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYDA 4
DB 19 SYDA 22
RESULT 44
ABB35934
ID ABB35934 standard; Peptide; 74 AA.
XX
AC ABB35934;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #3440 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
PD 09-AUG-2001.
XX